

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCGCAGGACCTGGAGCTCCGGCTCGTCTTCCCG
CAGCGCTACCCGCCATGCGCTGCCGCCGGCGCTGGGCTCCTGCCGCTTGCTG
CTGCTGCCGCCGCCGGAGGCCAAAGAAGCCGACGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAAACTTGGCGGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA
GGGCGACGGGTCTGCCGTGCCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAACG
GAAGATGCCCTGTGCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCCGACTTACCTTAAATTATTAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTGCAGTGGACAGCGCGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATAACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAGGGCGGCCGCACTAGACTTAGAGTCGACCTGCAGAACG
TTGGCCGCCATGGCCAACTTGTTATTGCAGCTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTCAAAATAAGCATTTCAGTGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAATCGCGCAGCACCATGCCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGCGAAAGAACCGAGCTGTGGAATG
TGTGTCAAGTTAGGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pi: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSDGSRQGDGSCRHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGTLTNRDCGECEVGWLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEEDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEAATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDGFHGPCKEAKLCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIKSKCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGGCTGGCGTCCGGCGTCCAGAGCCAGGAGGCCAGGCCGGGGCCAGCCTGGG
CCCCAGCCCACACCTCACCAAGGCCAGGAGCCACC**ATGTGGCGATGTCCACTGGGCTAC**
TGCTGTTGCTGCCGCTGGCTGCCACTTGCTCTGGGTGCCAGCAGGGTCGTGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCCGTGCCAGCAGCTGTGCCCTGCCAACCTGGCGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGCGTGCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
TCCAGTCTTGGGAACGTAAGTGGACAATGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACACAGCGCCTCTGGGCATGACCTGG**ATGAGGGATTGCTACCGCCTGGCACCA**
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACAGTGTGAACCCAGGGAG
GTGCTCCCACAGCCTCGAGGCCCTCTGAGAACAGTGGCCAAACCTGATTGATGAGCCTTTGA
CCAAGGCAACTGTGCAGGCTCTGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCTCGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCGCCGTCTCGATGGTGCCTGGTTCCCTGCCGTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGCCGTGAACGAGACGAGGCTGGCC
CTGCCCTCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAACGGCCCTGTCCAAGGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTTACAGGAGGACATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGAAAGGACGCTCAAATACTGGACTGCCAACCTCTGGGCC
CAGCCTGGGCAGAGGGCCACTTCCGCATCGTGCAGGCCGTCAATGAGTGCACATCGAG
AGCTTCTGTGCTGGCGTCTGGGCCGCGTGGCATGGAGGACATGGTCATCACTGAGGCTG
CGGGCACCACGCCGGTCCGGCTGGGATCCAGGCTAAGGGCCGGCGAACAGGCCCAATG
GGCGGTGACCCAGCCTGCCAGAGGCCGGCGCAGGCCGGCGCAGGCCGGCTAAT
CCCGGCCGGGTTCCGCTGACGCAGGCCGCCCTGGGAGGCCGCCAGGCAGACTGGCG
GAGCCCCAGACCTCCCAGTGGGACGGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCCTGGGCCCAACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCAAATCCCCTATTCTTTTTTTTTAGACAGGGCTTGCTCCG
TTGCCCAAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTC
AGTGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC
TAATTTTGATTTTGAAAGAGGGGGTCTCACTGTGTGCCAGGCTGGTTTCGAAC
CCTGGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAA
TAAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRADDC
ALPYLGAIKYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLLAGWEQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTTGACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACGCCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTCCTATAACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCATCCGCGCAGTGGCCTCCTGACCCTCATCAGCAAAGGCTG
CAGCTTGAACTTCGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTGGTCCTGAGCATTGTATG
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCTCTGTGCTGTTTC
CATGGCCCAGCATTCTCACCCCTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGGTGAGTGGATG
GGACAAGAGTCGACGTGAGTTCCGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAFSTLNPLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACGCGTCCGAAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCAGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATA CGGCCTCCAGAACGCCCGCACGAGG
GCTGGTTCATGGCCTTCACGCGCAGGGCGGCCGCCAGGCTCCGCAGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACGAGCAGTCGAGTTGTGGCTCCGCCCGGACCAAGCGCACAC
GGCGGCCCGAGCCCTCACGTAGTCTGGAGGCAGGGGGCAGCAGCCCTGGCGCCTCCC
CACCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTCCCGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTCAACCTGATCTAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTAGCGACTGAAGGCCTTGAGACAACCGTCTGGAGGTGGCTGTCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCGGAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCAACTCCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHKVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKS KDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTGACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTTCTGGACTTCACAGAACCCCATCCAGT
CATTTGATTTGCTGTTATTTTTCTTTCCCACACATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTCCCT
GAAGTCTTGGCTTATCATTCCCTGGGCCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATAATAATGC
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAACATGTCAGAGTTCTCCATTGAGGAAAAC
AATATTCAAGACCATTTCACGGGCTGCTTGCCTCTGAAGCTGAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGGCTTCCGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAACATCACCTGAGCAGTGTGCCTGTTGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCAGAA
TCTCACGAGCTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC
CACCCCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACCAAGAT
AAACACATTCCCTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTGATAATCTCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCTGGTTTGTGACTGCAGTATTAAATGGGTACAGAACATGGCTCAA
ATATATCCCTTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG
GGATGGCGTCAGGAATTAAATATGAATCTTGTCCCTGTCCTCCACACGACCCCCGGCTG
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCACTCAGCCTCCCACCCCTCTCTAT
TCCAAACCCTAGCAGAACAGTACACGCCTCCAACCTACCACATCGAAACTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC
CATTTGTGAATGATACTCCATTCAAGTCAGCTGGCTCTCTCTTCAACCGTGTGGCATA
CAAACTCACATGGGTGAAAATGGGCCACAGTTAGTAGGGGGCATGTTCAAGGAGCGCATAG
TCAGCGGTGAGAACACACTGAGCCTGGTTAACCTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGTTTAACCTACCGCGCGTAGAAGAACACCATTTGTTCAAGAGGC
CACCAACCATGCCCTCATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGTATCGGGGGCGCGGTGATATT
GTGCTGGTGGTCTGCTCAGCTCTTGCTGGCATATGCACAAAAAGGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGCGCGAAAGATGATTATGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAACACCAGTTTCAAGGCGTCTCCTAAATAACGAT
CAACTCCTAAAGGAGATTTCAGACTGCAGCCCATTACACCCAAATGGGGCATTAATTA
CACAGACTGCCATATCCCCAACAAACATGCGATACTGCAACAGCAGCGTGCACACCTGGAGC
ACTGCCATACGTGA CAGCCAGAGGCCAGCGTTATCAAGGCGACAATTAGACTCTTGAGAA
CACACTCGTGTGACATAAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTGCATTGAAATCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAAAGTG
CTATCTTCTATTCAAGTTAACACAGTTGTAACCTTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPSPHGAFFLKSWLIIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPaelHNQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLNTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPD
LPGTHLIRLYLQDNQINHIPLTAFSNRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARVELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTTSKLPTIPDWDRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATTTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVVLV
LSVFCWHMHKKGRYTSQWKYNRGRKDDYCEAGTKKDNSILEMTETSFQIVSLNNNDQLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGCCGGCGGAGACAGAGGCAGAGGCAGAACAGCTGGGCTCCGTCCCTGCCACGAGCG
ATCCCCGAGGAGAGCGCGGCCCTCGCGAGGCAGAGGCCACGAGGAAGACCCGGTGGCTGCGCCCCCTGCC
TCGCTTCCCAGGCAGGCCCTGCAGCCTTGCCCCCTCTTGCCTGCCTGCCAGGGAGCGGTACAGTGGGAGGTCCATCT
GCTTTCTGCTGATCCTCGGACAGATCGTCTCCTCCCTGCCAGGGAGCGGTACAGTGGGAGGTCCATCT
CTAGGGCAGACACGCTCGGACCCACCCGAGACGGCCCTCTGGAGAGTCTCTGTGAGAACAAGCGGGCAGACC
TGGTTTCATCATGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA
TCTTGCAATTCTGGACATTGGTCTGTGATGTCAACCGAGTGGCCTGCTCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGGTATAATGATCGTGAAGATGGGAGACCTCAGGACTCCGGCCAGGTGGCTGCTA
AGGCACGGGACACGGGCATCTTAATCTTGCCATTGGTGTGGCCAATTTCAGCCAGATTGAGAGCAGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGACGGCCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCACTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT
GTGCCATGGAGGACACAACGTGAGCAGCTCTGTGTGAATGTGCCGGCTCTTGTGCTGCCAGTGCTACAGT
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ATGAGTGTGAAATGCTGATGGCTCCTACCTTGCCAGTGCCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
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GTGTCACATGGGACAGATCCTTGCCCTGAGTGTGCTGAGGGACACGTGCTCCGCAGCGATGGAAGACGTGTG
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ATAATGGGAAATCCTACATGTCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGGTGAAGAAAT
GCACTGAAGGCCAATTGACCTGGTCTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAAATTTGAGGTG
TGAAGCAGTTGTCACTGGAATTATAGATTCCCTGACAATTCCCCAAAGCGCTCGAGTGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTCACTCTGAGAAACTTCACAGCCAAAGACATGAAAAAAGCCGTGCC
ACATGAAATACATGGAAAGGGCTCTAGACTGGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTCACCGACGGACGGCTCAGGATG
ACGTCTCCAGTGGCCAGTAAAGCCAAGGCCATGGTATCACTATGTATGCTGTGGGTTAGGAAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCCTGAGCCCACAAACAGCATCTTCTATGCCAGACACTTCAGCACAATGG
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CAGGGGAACGTCCAAAACCGTCCACAGCCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTTCAGTGCAGTGCACACAGATATCTGTTGAGAAGAGACAATCTTACGGCTCACACAAAGCTTT
CCCATTCAACAAAACCTTCAGGAAGCCCTTGGAAAGAAAAACACGATCAATGCCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAACAGAAGAAGTAAAGAAAATTAAACACAGGCCCTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATCGCCTGAGATAAGATGAGATTAGAAATCGCGACACATTGTTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAACAAATCAGTACTGA
GAAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATAACACTAATGTATAATTCTAGGAAAAAAACCT
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCCAGTATTGTAATATACTGTGGACAC
AACTGCTTCTGCCCTCATCTGCCCTAGTGTGCAATCTCATTGACTATACGATAAAGTTGCACAGTCTTACTT
CTGTAGAACACTGCCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGGAACAAGTTGATTTTTACAAATATTAAACCAACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRRHARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINI PGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVRLSDGKTCAKLDSCALGDHGCE
HSCVSSEDASFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVKSTHGCEHICVNNNGNSYICKCSEGFWLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDSILTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTTINIQDLLSCSNFAVQHRYLFEEFDNLRTQKLSHSTKPSCGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCGGCAGCCTCCGGCGTGCAGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGGGCTGGCGCCCTGACTCCGTCCGGCAGGGAGGGC
CATGATTCCCTCCGGGGCCCTGGTACCAACTTGCTCGGGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCTCGGGCCCAGCTGCAACTGCACCTGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTCTCCAGCGTGGTACACCTGCACGGGAGGTGCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTCACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCGGAACCTGTCCTGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCATACCA
GTGGGATCGGAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGACTGCCAATGTAATGTGACGCTGGAAAGTGAGCACAGGCCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTTGACTGGCTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCAACGCCGGCAAGGCCCTGGCCAGGCCAGCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCATGCCCTCCAGGCCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTCTGGTAT**GATGAC**
CCCACCACTCATGGCTAAAGGATTGGGCTCTCCCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCTTAGTACTCTGCCAACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCTCCCAGGC
CCCCTGATCTGTAACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC
TTATTAAAAACTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATAACATAA
TGTTTGATGAAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTLWPKSSDTISKNGTL
SSVTSARALRPPHGPPRGALTPTPSLSSQALPSPRLPTTDGAHPQPISPPIPGGVSSSGLSR
MGAVPVMPVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACGCCAATGAAACGCCTCCGCTCCTAGTGGTTTTCCACTTTG
TTGAATTGTCCTATACTCAAATTGACCAAGACACCTTGTCTCCAAATGAAAATGTGA
AATACGCAATGAAATTGAGCCTGCTATTGCAACATGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGTCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAACTTAAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTGTAACAAACCGTGAAT
AATTGTTCAAAGGGATACATTGTAGTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTAACAAACTCATGCACACTGTTGAACAAAGCTACTTTAAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTTGAT
TCATATAACATGAAACATATTCACTCATATGAATATGGATGGAGACTACATAAATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGTCCTTGCTTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACATTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTTCGAATTGGATGTCCTCTGGCTTCCATTGGTATTAAAGATTATAATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTCITGCCATATGCATT
ACCTTCTGGTTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAATCTTGCTG
TAGCCTATTCTTGCTGAACCTGTTCTTCTGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATGCCGACTGCTACACTACTTCTTTAGCTGTTGATGGATGTGC
ATTGAAGGCATACATCTATCTCATTGTTGGGTGTCATCTACAACAAGGGATTGGCA
CAAGAATTATATCTTGCTATCTAACCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTGGCACACCAAAGTATGTTGGCTTAGCACCGAAAACAACATTATT
TGGAGTTTATAGGACCAGCATGCCAATCATTCTGTTAATCTCTGGCTTTGGAGTCAT
CATATACAAAGTTTCGTACACTGCAGGGTTGAAACCAAGAGTTAGTTGCTTGAGAAC
TAAGGTCTGTGCAAGAGGAGCCCTCGCTCTCTGGCTTCTCGGCACCACCTGGATCTT
GGGTTCTCCATGTTGTGCACGCATCAGGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTCCAGGGATGTTCATTTTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAATGTCCCCTGTTGGATGTTAAGGTAAACATAGAGAATG
GTGGATAATTACAACGTGACAAAATAAAATTCCAAGCTGAGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTAAACTACTAGACAAAAAGTATTAAATCAGTTCT
GTTTATGCTATAGGAACGTGAGATAATAAGGTTAAATTATGATCATATAGATATACTATGT
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGAGATATTGAAAGTAATTGGTTT
CTCAGGAGTGTATCACTGCACCCAAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCAGTGGCTGATATTCTGTGACTCGTGTGCTTGGAAACTAGTCC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAACAGAAGGG
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTGAAATGAACTGTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTACCAACGAGAAGTATATGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTTCTGTTGCTAAATCTGTTCTT
TTCTAAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTESYYCMCVPGFRSSNQDRFITNDGTVCIENVANCHLDNV CIAA
NINKTLTKIRSIKEPVALLQEYVYRNSVTDLSPTDIITYIEILAESSSSLGYKNNTISAKDTL
SNSTLTERFVKTVNPFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSYNMKHIIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSIAGL
LHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVGFSAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLVHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCTTGTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTACCTC
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTGGGGCCGCTGCCGTGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCCTCCCGAGATCCGAACGGCCTGGCGGGGTCAACCCGGCTGGGA
CAAGAACGCCGCGCCTGCCCTGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
GGTGTGAGTGGGTGTGTGCCGG
TGTCTGGGCACCTACCCGTGGGGCCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCCGCGCGTCAGAGCAGGAGCGCTCGCTCAGGATCTAGGGCCACGACCATCCAAACCC
GGCACTCACAGCCCCGAGCGCATCCCGTGCCGCCAGCCTCCCGCACCCCCATGCCGG
AGCTGCCCGAGAGCCCCAGGGAGGTGCCATCGGAGCGGGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGTGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
CCACGTGCACTACGGCTGGGGGACCCCCTCCGCCTGCCGACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCCCTGCCGCATCCGTGCCGACGGCGTGTGGACTGCCGCCGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCGACCGTGGCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCAGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCGGTCTCCCTGAGCAGTCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCATTTCTGCCCATGCTGCCCATGGTCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAACT
GAGACCATGCCGGGCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGCTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCAGTTCTAGCCATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGCCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACTTCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGCAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTCACTCAACCCATGTGGGATTGATCTATCTACTTCCAGGG
ACCATTGCCCTTCCCAAATCCCTCCAGGCCAGAACATGACTGGAGCAGGCATGGCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGGCCACTCCAGCCCTGGGACAATTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTGCTGTCCGGTGTACCTGC
TTCCATCTCCAGGCCACCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGGCCT
CCCAGGCCCCCACCCTATGTCAACCTGCACCTCTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTGCTGTGGAAGCAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAAATTATTTATGTATGTAAGTGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEET
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGAACCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCACCGCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGACTACCAAGAGGCTATTTAGCCTGAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGTCTCCTTGCTAC
TATCAACAGACTCTCAAGGTATTAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGAGCTGCCCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACTGACTCTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCGTGAAGCCGCAATT
TGTTGGATATCGCAGGTGCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTAAAAATGTGCAGTGGCTACGCCTGTAATCCCAGCACTTGGAAAG
CCGGCGGGCGGATCAGGAGTCAGGAGTTCTAGACAGTCTGGCCAATATGGTAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGGATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAAATAAAATAATA
AATAAAATACTGGTTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGLRLLENPRLGSQST
NSSYTMNTKTGTQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIIAAVVVVA
LVIISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCCACAGCCCAGGCCATGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCACATCTACATACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAAGGAAATAGTAACCTCTTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAAACTTGTGGTCTATGGCATTCA
TTTGACAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG
TGGAACTCTTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCACAGACTAACAAATATTGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGA
ACTGCCTGAAAATGTCGTCCGAACGTGAGCAACTTACAAGAACTCTATATTAAATCACAACT
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT
TCTGATGATTGGGGAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTCTTATCA
ATCTTCGCGCCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCGATAACGCCTGGTT
GGACTGGAAAACCTTAGAAAGCATCTCTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAACCTTATTAAATAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTTAAAGAGTTGGGATAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACAAACCTAGATTGTCTTACATTCAACCCATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGAGTCTCG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG
GATGAACATGAACAAAACCAACATTGATTGAGCCAGATTCACTGTTTGCCTGGGACC
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTCAAGGACATGATGGAAATTGT
CTCCCTTCTTATAGCTCCTGAGAGCTTCTTAATCTAAATGTTAGAGCTGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAACTACTGGATAACACCTTCTG
GTCAAAACTCTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAATGGCGTAACCTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCAATTCACTGTTGGTGTCTGGAAAGCA
AGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAATTCTCA
TGCTGCGCAAAGTGTGCGAATACCATCTGATGTCAAGGTATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA
TGTGTAATGTCAACCACCAAAGGTTGCACCCCTGATCAAAGAGTATGAAAAGAATAATAC
CACAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCCTGTGATAAAATCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCCT
AAAAACCAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYSTDFFPVNLTGQLDSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLSNRQLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFLLDKNPINRIRRGDFSNMLHLKELGINNMPELISIDS LAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSA LYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFM EPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNTTKGLHPDQKE
YEKNNTTTLMACLGLLGIIGVICLISCLSPEMNCDGGHSYRNYLQKPTFALGELYPPLIN
LWEAGKEKSTS LKV KATV IGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTAACCGTTCCCTCCATGTGTCCTCCTACAAAGTTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCTAACAGGCTGTCTTGTCTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTTTAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGGATGAAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGTTGGCTGGTTCACTATGGTATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAACGAGGAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTGCAGTGCAGTAGAAATAAGTGGTTACTTCTCCCATCATTGAAACATTTGAA
ACTTTGTATTCAGTTTTTTGAATTATGCCACTGCTGAACTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCATGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLSDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNICKTSVLDEHAGRPFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCCGCCCCAGATGCAGGTGAGCAAGAGGATGCTGGCGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATTCTCCTGCTGGTGC
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCGCCCCCTGCGAGTGCCTCCGCCAGG
ACCGCCTGTGCTGCCACCGCAAGTGCCTTGTGGCAGTCCCAGGGCATCCCCACCGAG
ACGCGCTGCTGGACCTAGGCAAGAACCGCATAAAACGCTCAACCAGGACGAGTTGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTAACGAGAACATCGTAGGCAGCAGGCCGG
CCTTCAACAAACCTCTCAACCTCCGGACGCTGGCTCTCCGAGCAACCGCTGAAGCTCATC
CCGCTAGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCCTTCAGCGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT
CATCGCTTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGTCCGCCACCTAGTCTATCTCGCTCCTCAACCTCTCCTACAACCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGGAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGGCCTCAACTACCTGCGCGTGCCTCAA
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTCCACTCGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCGCTGGCCTGCAGTGTGGCTCTGTGGGTGTTCCGG
CGCCGCTGGCGCTCAACTCAACCGCAGCAGCCACGTGCGCCACGCCAGGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGGGCCACACGGTGCAGTT
GTGTGCCGGGCCGATGGCGACCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGGCCCATCAGCCAAACAA
GACCTCGCTTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCCGCCACTG
TGCCTTCCCCTCGACATCAAGACCTCATCATGCCACCCATGGCTTCTCTGGAGCCGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGCGGGGGCAGGGACCCCG
GGCGCCGGGAGGGGAAGGGGCTGGTCGCCACCTGCTCACTCTCAGTCTCCACCTC
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCCGTCCCCTGCTGCCCG
CCAGCCCTCACCACTGCCCTCTTCTACAGGACCTCAGAAGCCCAGACCTGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA
ATAATTCAATAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTCAATAATTATGGATTT
TATGAAAACCTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTTLIESVFHSVGNLETLLIDSNPLA
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKNSNGRLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

DRAFT: 07/11/02

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCTGCTCCTGCTCCTGC
TGTTCGCCTGCTGCTGGCGCCCGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGTGCCTAAGTGCCTAAGTGAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCCCTGCTCAGCAGACTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAAGCTGGTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTTCAATTACGGAAAAAGACACAGCCACCCCTAAACTGTCACTTCTGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCACTGAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCAGAAGCTGTTGCTACACTGTGAGGGTCGCGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCGTGGATCGTGGCTTCATTGTCTTCCCTGCTG
CTCATCATGCTCATCTTCCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCATCTAGGCGCTGCCACTTCCCTGC
GCCCGGGCAGGGCCCTGTGGGACTGCTGGGCCGTCAACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGTCTCCAGCCACCCACCCCCCTGTACAGAAATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAACA
AACAAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVAGGTVVLCQVKDHEDSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCSIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAATGCCTTGATTCTGTT
GCTGGAGACGTCTCTTGTGCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTCCCAGTTTACCATTTATTCTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTCTGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCAGGCTGATTAAATTATTACGAGATATAGACCCGGGGCTTCAGG
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGGAGATCCTGCTAGAGGATAACCCTT
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGCTCGCAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCCAAGAACAGAGACCTTGCTCTGGACCCCTGCCAACCTCCTTAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCGAGCTGCGACCACATCCCAGGGTGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCTACGGAGATAACAAGATCCACAGCATCCGAAAATCGACTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCCGG
GAAATTCGCGGGGCTGCAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACAAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCCGTGGCAGGGTGGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT
TAGAAAGGATTTCATGCTCCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACCTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCCGGACTGCTGCTGGT
GTTTGTCACTCCGCCTTCACCGTGGTGGCATGCTGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGAGCAGAGATGCCAACCTCCTCCCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GAECTCTCCTACTGGCACAATGGGCTTACAACGCACTGGGCCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGCCCAGCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCTCGCCCTCGGCCCCGGGGCTGTGGGGTTGGATGCCGCGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTCVCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTA
FYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNLHEIVPGAFGLQLVKRLHINNN
NIKSFRQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVILNDNLISTLPANVFQY
VPITHLDLRG
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNA
LIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLAPPQA
ETFAPGPLPTPKTNGQEDHATPGSAPNGGT
KPGNWQIKIRPTAAIATGSSRNKPLANS
LPCPGGCSDHIPGSGLKMNCNNRN
VSSLADLKPK
KLSNVQELFLRDNKIHSIRKSHFDYKNL
LILDLGN
NNIATVENNTFKNLL
DLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNAIQL
LIPGTFNAMPKLR
LILNNNLLRSLP
VFDVFGVSL
SKLSLHN
NYFMYLPVAGVLDQLT
IIQIDLHGNPWECS
CTIVPFKQWAERLGSEV
LMSDLKC
ETPVNFFRKDFM
LLSND
EICPQLYAR
ISPTLTSHSKN
STGLAETGTH
NSYLDTS
RVS
ISV
VPGLLL
VFVTSAFTVV
GMLV
FILRNR
KRSKRR
DANSS
ASE
INS
LQTVC
DSSYWHNG
PYNADG
AHRVYDCGSHS
LSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCCCTGTGCGGGCTAAGGGAAACTGTGGC
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGGTCCGTCGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTGTGGAGCAGCTCTGCGTGCCTGGCCTCAG
AGAATGAGGCCGGCGTTCGCCCTGTGCCTCTGGCAGGCCTCTGGCCCGGGCGG
CGGCAGAACACCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGCGGCCAGGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGCTGCCTGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCAGG
GCCCGGAGGGGCTCAAAGACCTGCTGTTCTGGGTCGCACTGGAGCGCAGGCCTCCCAGT
GCACCCCTGGAGAACGAGCCTTGCGGGGTTCTCCTGGCTGTCCTCCGACCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGAGGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCAGTGGGTCGAGCCCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGTACCTGTCAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCGG
GCCGCCTCTAACCTGAGCTATCGCGCCCTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTGCGCTCGCCGGGACAGCTCCGATCTCAGTTACTGCA
TCGCGGACGAAATCGGCCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCC
GGGAGGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTGGGAGG
CTTGCGCTGCGAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCCGCTCTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGGACCGGGTGCCCACCAGGGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGCCAATCAGGGTCGACGAGAACGACTGGGAG
ACCACTGTCCCTGAACAAGACAATTCACTAACATCTATTCTGAGATTCCCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTTCCTCTGCCACTCCCTCAGGCTT
CGACTCCTCCTGCCGTGGTCTTCATATTGTGAGCAGCAGTAGTAGTGTGATCTGGGAG
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAGAAAGCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGATCCTGAGCCGCTGCTTGGGCTC
CAGTTCTGCACATTGACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTGCTGGGGAGTCCCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACAGGGGAACCAAGAGGAACATTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAGTGCCTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGAGAGATATTCTTATGTTATCGGAGAA
TTTGGAGAAGTGATTGAACCTTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCYQFEVLCAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGFFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTSSATPQAFDSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACCCGTGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG
CGTCGAGTCAGACGGCACATAATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGTATC
CCCCGGCTACCTGGCCCGCCCCGGCGGTGCGCGTGAAGAGGGAGCGCGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGTGGGTGCGGA
GGGGCGTGTGCGCCGGCGCGCCGTGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGCTGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGAAATCA
CAGTTCCCAGAGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTACAATGCCATGCCAATGCCAGCGCATTGGCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAAGTGGCAGACCGGGATTACCCCTGCAGGAGTCAGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGGGGGAAAGTCACCGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCGCAATTGTGTCTGAGAGAAATGAACCTTATTCACT
TTTATCAGACTTAAGTTAAC TGCAAGATGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACACTACAGAACAGCTGTCAACCACATTCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCCTGTGCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGCACTGTTATCACACCATCACTCGCGATGGGAGTTG
CACGCCACAGTCTGATCATCACATCTACAAAGAGGGAAATTGGCGATTCAAGAGGGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACAGACTCCTGGATGCCCTAAAAAATAAGCAATG
TTAACAGTGAACGTGTCATTAAGCTGTATTGCCATTGCCATTGAAAGATCTATGTT
TCTCAGTAGAAAAAAACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GAATGGTTGACTCTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAAGAGGAGCAGCTATCTGATTGGAAACCTGCCACTAGTGCCTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTATTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTAGAAGTGCAATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGTCTGCCTTCTA
AATCAATGCTTAATAAAATATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYPAVGTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRGTLEGN
YCSSLDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGGCGTGGCGGGACCGCGTGGCGGCCACGGCGCCCGCGGGCTGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTCTCCCCGCCTCAGCCCCATCCGTGTCATAACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACACTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGAACCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTCACAAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAACCG
GACACGAGGGGGCAGCAGGGCACTGTGACTGCCAACGCCAGGGCTACGGGGGTGAGGCCTGTC
AGTGTGGCCTTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAACGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTCGTGAACACTGAGGGCCTCATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTTGGTGTTCACGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAAGCGCAGTGACCGTGTGGCTGGAGGGCTCATCAAGGGCAGA
TA
ATCGCGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCC
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAA

FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPAGTERPCGGYQCEGEGRGGSGHCDCQAG
YGG EACGQCGLGYFEAERNASHLVC SACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACL GCMAGPGRKKCSPGYQQVGSKCLDVDECE
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWL SERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA
GCACCATGCCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGTCTTCAGG
AGCCGGTCCCCAAGGCCCGCCTGCACAGGCACGGGCGCTGTCCCCCGCGCAGCGCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGCACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGGCCAACAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGCCGAGAACTGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTAAGTGGC
CGTTTCTGGGCCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCCTGGATGGTGCCTCGTGCCTAGGCCAAGGAGGCTCAGCCATGGCGCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGGCTCTCAGGAATGAGAAATCTTGCCACTGG
GAGCCCTTGCTCAGTTCTCTATTCTTATTCACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCTCCACCACCTGGACCTAACAGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAAACACATTATTCT
AAAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDGDPPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGAACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGTGCCTACGAATCCAAAAGCACCCGTGCCTTCAGCAACTCTCCTATGTCC
GAATCCCACAAACAGGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATACTGGAGAACATA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAACAAACAG
ACCTCGTCATTCCCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCTTC
TACACCCCACAGGGCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTTAAA
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTTGGTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGCTCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACGGAGCTGGGCGCAGTGGCTACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPEENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIIVMPTNPKSTRAFSNS
SYVLNPTTGELEVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAABLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCCGCGTGGCCGGCGCCGCTGTGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTCCCACCCACCAAGTCCAGTGCCGACCAGTGGCTTATGCGTGCCCCCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGTGCACGGCCA
CCCAGACTGTCCCAGTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG
GGGATGCCACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTACCGCCACCCCTCCCTTTGTCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAC
CTCGCTGCCTGAGGACAAGCACTTGCCACCGACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLD CSDGSDEEECRIEPC TKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNC SRLA CLAGELRCTL SDDCIPLTWRC DGH PDCPD SSDEL GCGTNEILPEGDATTMGP PVT
LES VTS LRN ATT MGPP VTLES VPS VGNATSSAGD QSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLG LLLVAMKESLLLSEQKTS LP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACCGCGTCCGGTCTCGCTCGCGCAGCGGCCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCCGCATTCCGAGAATGGCTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTGTGATGAAGGATTCAAGATCCGG
TACCCCCGACCTACACAATATGGTTTCAATTATGTCGCGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTGTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCAGCCCACCCGGTG
CTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCAATGGTGAGTCACGGAGATTCGTCT
GCCACCCGCGGCCCTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCCCTCCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTGGTAGACGGCGTGCCTCATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGGTTGAGTGCCTTAGGCCCGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTCGGACAACCTGACATA
ATTGCCAGCAGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAATTTCCAAAGTGTCTGAAGTGTCTTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTTGGTTTAGACAAATGTAAACAA
AGCTCTGATCCTAAAATGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTCTTGTGACACAGACTGATTAATAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKAGTKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLVILARMFQTKFAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCGTCCGCTCCGGCCCTCCCCCGCCTCCGTGGTCCGTCGGTGGCCTAGAGA
TGCTGCTGCCGGTTGCAGTTGCGCAGCCTCTGCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCCGCTACAGG
CCGTGCTGCTGCCGTGCTGGTGGGCCGACGGTCGCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTAA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACATTGAGGAAGCCAAGAACGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTTGCATCTGATGGTACCTCTGGATTGGCTCAGGAGGCCTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT
CACAATTTAGGAACGGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTGGTGGTCATG
TACCATCAGCCATCGGCACCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTTCATTGCAAATATTCTGATGAGAAACCAGCAGTTCC
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAACATTAAAGAAAGTAGAGAAGCTGCCCTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCTTCTCCTCCTGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACCAC
TGGCCCTCTCCTCACCAAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAATATTCAATTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTTATGA
GTTCTCCCCAGACAAATGGGAGGAGTAAGGAGTCTGGATGGCTGAAAATGAAATATATG
GTTATTAGGACATATAAAAATGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCATTGGTTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAGATGGCTGTGGAGCTTGGAAAACCACCTCTGTTCTGCTATACAG
CAGCACATATTATCATAACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTCAAAGAACATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNIALYILIPSIPLLLL
VTTVVVCWVWICRKRKREQPDNSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSQDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGGTACTGCCTGCACC
AGCGGCCGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCAGCAGC
CTGCTGAAGTTAAAATGGTGCAGGTGTTGACACCGGGCTCGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAAGTCTGTATCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCCT
GGACAACTGCTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCAAGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSFYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTAQLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHLPLSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAA
ACTAAATATGCTGCTTGGGGACCTCCTTAGCCT
TAAATTTCAGCTCATCACCTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCCTGGTGGGGGCCT
CCACCGCTGTGAAGGGCGGTGGAGGTGGAACAGAAAGGCCAGTGGGCAACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCCCAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAAGAACAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTGGGGAAAGAACACACTGCAACCAGATGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA
CCAGGGTGGTATGCAAGCAACTGGGCTGTGGAAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTGGGGTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGGACTTATACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGAACTACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTTGTCTGTTCTGAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAAAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGLASPSGVRLVGGHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL
RELGCAGASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCGSRLEVHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGTCCGGACCGTGGCGGACCGTGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG
CGTCTCGGCCTTCCGGCTGCTGCAGTGGTGCGCGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCCACCTCAGGGCTGGCAAAGAAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCCTGTCAGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTACCTCGACC
TCACAGACTCTGGGCCATAGTGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACAGTGGA
TGTGGACAAGAGGGTCAAGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGGCAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATACCGCGATGGATCTAGGTATGGAGTTATGGAC
ACCACCCACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTCAGCCTCATGGCCTCCAGGGCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGGCCAGGGCAGAGAAGCAGCACTCTTAGGTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTACAAGTGG
AAAGACTGAAGAAACACATCTGTCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAACAGTAAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDFATQDPQIEKTFEVNVLAFWTTKAFLPAMTKNNGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCCGCGGACCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTCGCCGCACCCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCTGGCCCCGTGATGGGCTGTTCGCTCCCTATAAGAAGT
GTTTCCATGCCACCTAACGGAGACTCAGGACAGCATTATTCTCACCCCTAACATTGAAGC
TGGGAAGATCCAAAAAGAAGAGAAATTGAGTTGGTGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC
TTCCCAGCTCAGATAACAGCCAGAACAGATGCCAGTAGTTCTGGTACAGGGTGGCCGG
AGGTTCATCCATGTTGACTCTTGTGGAACATGGCCTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTCAGTAATTCACTAGTTTCCAGATAATTCTGAATATAAAAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCAGAACATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGGTGGATGAGAACAAAAAGTACTTCCAGAACAGCTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGTTAAC
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGAAATTGGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAAGTACTTGCAGA
AGATAACAGTACAGTCAGTTAACGCACTGGTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAACGGAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGGGGTGACTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTACCTATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCATTATGGAAAAGGATGGATCCTTATGTTGATAAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATGTAaaaACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTTCTCATCAATAAAAATTATCCTTGAAACAAGTGAGC
TTTGTGTTGGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAATGA
AATTTAGGGTCTGAAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAAGCTTAGAACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL
VGPFPGGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLDRDFPWTTTLSMLYIDNPVGTGSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPKREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTCCGGCTCCGAATGGCACATGTGGAATCCCAGTCTTGTGGCTACAAACAT
TTTCCTTCTTAACAAGTTCTAACAGCTTCTAACAGCTAGTGATCAGGGTTCTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGAAAG
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCCTAACAAAGCTTCAAAAAACAGGAGCGACTCCACTGGCTGGAT
AAGACGTGCCGGTAGGATAGGAAAGACTGGTTAGTCCTAATATCAAATTGACTGGCTGG
TGAACTTCAACAGCCTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGCCAGAAA
TAGAGATGTTGAAAATAAAATTAAAAAGCAAGTATTTATAGCATAAAGGCTAGA
GACAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGAGAAAGTATGTTAAAATA
GAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCAACAGGATGGGACCCCTGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCCTCTGCCTTGTGTTT
GCAGAATCATGTGAGGGCAACCGGGAAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCAGTGGTCTGGGTGCTGGCCCCCCCAGCAGCCGGC
ATGCCTCAGTTAGCACCTTCACTCTGAGAATCGTACTGGACCTTCAACCACCTGACCGT
CCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATTAAGACAGGGCCAAGAGGACAACAAGTCTGTTACCCG
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGTCTCACCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTCATCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTCATCGGCACGGCTGTGGATGGAAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCTCTCCACTTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCCCGAGA
CCCCTGAGGGTGTGGCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGG
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCCTGCCCTCGGCTGCACCCGGC
CGGGGTGGAATACCGCCTCTGCAGGCTGTTACCTGGCCAAGCCTGGGACTCACTGGCC
AGGCCTCAATATCACCAGCCAGGACGATGACTCTTGCATCTTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGCTGCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGCGCTGTCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGTAAGAGTCTATGAGTTAGCTATTGGTGGAGATTAACTATAG
GCAACTTTATTTCTGGGAACAAAGGTGAATGGGAGGTAAGAAGGGTTAATTTGTG
ACTTAGCTCTAGCTACTCCTCCAGGCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCACCTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYWSDHSALCFAESCEGQPGKVEQMSTHRSRLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNVNKLIIIDYSENRLLAGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEQN
LELNWL LGKD VQCT KAPVP IDDNFCGLD INQPLGGSTPVEGLT LYTT SRDRMTS VASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEG SYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCCGGCTGAGTGGACTGGAGTGGAAACCCGGTCCCCGCGCTTAGAGAACACGCG**ATGACCA**
CGTGGAGCCTCCGGCGAGGCCGGCCGACGCTGGACTCTGCTGCTGGTCGTCTGGCTTCCCTGGTGCCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCCTGCGGCTCCGCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTCGGGGCTCCACTATTCCTGTCGCCCCAGGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCTGTTGAACACCCCTACCCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAAGAGGCAAATTGACTTCTCGGAAACCTGGACCTGGAGGCTTCGTCTGATGGCCGAGAGATCG
GGCTGTGGGTGATTCTCGCTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGCTTGCCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTAACAGGGCTTACCGAAGCAGTGACCTTATTTGACCACC
TGATGTCCAGGGTGGTGCACCCAGTACAAGCGTGGGGACCTATCATGGCCGTGCAAGGTGGAGAATGAATATG
GTTCCATAATAAAGACCCGCATAACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGGAACCTGC
TCCTGACTTCAGACAACAAGGATGGCTGAGCAAGGGATTGTCAGGGAGTCTTGGCCACCATCAACTTGCAGT
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTCAACGTCCAGGGACTCAGGCCAAGATGGTATGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTACAATATCTTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGCTCTCCATCAACCTTACATGTTCCACGGAGGACCAACTTGGCTTCATGAATG
GAGCCATGCACTTCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGTCGACAGAAGCCGGCG
ATTACACGCCAAGTACATGAAGCTCGAGACTTCTGGCTCATCTCAGGCATCCCTCTCCCTCCCCCACCTG
ACCTTCTCCCAAGATGCCGTATGAGCCCTAACGCCAGTCTGTACCTGTCGTGGACGCCCTCAAGTAC
GGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATGGGGCAGG
TGTTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCACTATGGGGAGAATTGATGACAGCGCAAAG
GCTTAATGAAATCTCTATCTGAATGATTCAACCTCTGAAAACCTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTTGG
GTAGCTTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGTTGTATTCA
TCAATGGCCAGAACCTGGACCTACTGAAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACAGGTATCGTTTGAGGAGAGATGGGGCCCTGCATTACAGTTACGGAAACCCCCC
ACCTGGCAGGAACCAAGTACATTAAGT**G**AGCGGTGGCACCCCTCTGCTGGTGCCTGGAGACTGCCGCCTC
CTCTTGACCTGAAGCTGGTGTGCTGCCCTCACGCTCAAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCCCTAACGCTGCAGGGAAAGGTGGATGGCTCTGGGCC
TGGTTTGTGATGATGGCTTCTTACAGCCCTGCTCTGTGCCAGGGCTGTGGCTGTCTAGGGTGGAGC
AGCTAATCAGATGCCCTGGCCCTCAGAAAAAGTGTGAAACAGTGCCTTGCAACGGAGCTCACAGCCC
TGCAGCATCTGCTGGACTCAGGCGTGCTTGTGGCTGGGAGGCTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTGT
CTTCCTTACAACCTTCTGAGCCTTCTTGGGATTCTGGAGAACACTGGCGTGAGAAACATGTGACTTCCCTT
TCCCTCCACTCGCTGCTCCCACAGGGTACAGGCTGGGCTGGAGAACAGAACAGAACATCCCTCGTCTTCC
CAAGTTAGCAGGTGTCTGGTTCAGTGAGGAGGACATGTGAGTCCTGGCAGAACCCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCA
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCA
GGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCA
ACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCAGAGCAGGGCAGAGCAGCCCTCTTC
GAAGTGTGTCAGTCCGATTTGAGCCTGTTCTGGGCCCCAGCCAAACACCTGGCTTGGCTACTGTCTGA
GTTGCAGTAAAGCTATAACCTTGAATCACAA

FIGURE 64

MTTWSLRRR PARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLMKACGLNTLTTYVPWNLHEPERGKFDSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVIDLYFDHLMMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDKGLSKGIVQGVLAT
INLQSTHELQLLTTFLNVQGTQPKMVMEYWTGWFDSWGPHNILDSSEVLKTVAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLDRFFGSISGIP
LPPPPDLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNQSFYIYE
TSITSSGILSGHVHDRGQVFVNNTVSIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSPKLNFRYISLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACCGGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCAATGTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCT
CCC
AAGAACGCTGTCCGTGCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGCTCGTAGTGGATAGGGTCACTGACCGGTTCTCCTAGACGGGCC
CGTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGGTACCGCGGGTGTCTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAAGGACCTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCATCCTGGTTGCTTCGAAAACCTGAAATTCACTAAGAACCTC
AGATCCAGACTCCTGCCGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCAAGATATATC
CATGGCTTATACACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTCGTGCACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GAECTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCATGGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGACCCCACACCTAACGTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCCTAGACTTGCTTGGCCCCGTGGCCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAATAATGGAGTC
CATGACCGTGCCTATGTGATGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTTGACGGGAAACTGGGTCAAACACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGCTAACAGCAGTGACTCAAGGGCTGTGAAGCCACCAATTCTG
GGCAAACAATCCTAACCAACTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCCTCCAGTGCACAAATGCCATATCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCAAGTCTGGATCAATGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCCTAGGGAGCCCTCAACAAAATTA
CATTGCTGGAACCTAGAAGATGTACCTCTCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACTTGAAAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAACACCCGTCTCCACTAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAACCTCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIIISIQVENE
YGSYRACDFSYMRHLAGLFALLGEKILLFTTDGPEGLKCGSLRGGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSAADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGACACCTTGAAGGAATATT
CTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT
GCGTTCTTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCA CGAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTGGGGGTGCCGATGCTGTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTCAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAATTACAGGAACTGGAT
TTAAAGTCCAATAAACATCGCACATTGAGGAAATCATCAGTTCCAGCATTAAAAGACT
GACTTGTAAATTATGGATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTCTAACAAACAGCTCGAACCTTACCAAGTGGCAGTATT
AGTTTACAGAAACTCAGATGTTAGATGTGAGCTAACACACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGGACAGAACTGCATCACC
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGGT
TGGAGATCACCTTTGATAACCCTGCCACTCGAAGTCAAAGAGGGATTGAATCAAGACATA
AATATTCCCTTGCAAATGGGATTAAAACTAAGATAATATGCACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAACAGAGAGGATGCATAGAACGGCTGATAGAACAGACATAACTGAAT
GTTCAATGTTGAGGTTTAAGTCATTCTCAAATCATTGTTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESIRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

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Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACAGCGTCCGGCCTTCTCTGGACTTTGCATTCCATTGACAAACTGACTTTTTATTTCT
TTTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCGCCCTGGGAAGAACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTTCCCTCCCCTGACATTGGCATTGCTTAGTGTTGTGTTGGGAGGGAGACCACGTGG
GCTCAGTGCTGCTTCACTTATCTGCCCTAGGTACATCGAAGTCTTTGACCTCCATACAGTGAATTATGCCCTGTC
ATCGCTGGTGGTATCCTGGGCCCTGCTCCTGCTGATAGTTGCTGCTCTGTCTTACTTCAAAATACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGCTGTAAGGATCAACACCAGACAAGGTGTTGGGGCAAG
AACAGCCAGGCCAAACATTGCCACGGAGTCTTGCTGCCAGTGCTGTGAAGGATATAGAATGTGTGCC
AGTTTGATTCCTGCCACCTTGCTGTCACATAATGAGGGCCTGAGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGGCCCTGAAGACTTCATGATGTCATGAGGCCACCTGTTGTGATGTCAGGCACAGAAGAAAGGCACAG
CTCCCCCATCAGTTCATGAAAATAACTCAGTGCTGGGACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCCCTCACTGTGGGAATGCTGATAAACAGTC
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAACGTACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGGCCATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTCTTAATTCTCTCTGTTGGCGGAGCTGACAATGGCGGAGGCTGAAGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTCCATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTAAAAGCTTGAACGGAACTCCAGCAATGGGCTCTGCTAGGG
CAAGCTGCAGTAAAACGACTATGTTCTGTATTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GAECTCAGCAAGAATTCAAAGAACTGTCTTGTCTTACTACTTCTCTCTCTAACTCTCTATTCCAAACTGT
GGCGGTTACCTGGACACCTTGGAGGATCCTCACAGGCCAATTACCCAAGGCCATCTGAGCTGGCTTAT
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTCAAATTGATTTCTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCGGTGTGACTCCCACCTTCAATCGTCATCAAACCTCTGACTGTCGTGTTCTACAGATTATGCCAATTCT
TACCGGGGATTTCCTGCTCCACACCTCAATTATGCAAGAAAACATCAAACACTACATCTTAACCTGCTCTT
GACAGGATGAGAGTTATTATAAGCAAACTTACCTAGAGGTTAACTCTAAATGGAAATAACTTGAACAAAA
GACCCAACTTGCAGACCAAAATTCAAATGTTGGAATTTCCTGCTCTTAAATGGATGTTGACAAATCAGA
AAGGTAGAAGATCAGTCATTACTACACCAATAATCACCTTCTGCATCCTCAACTCTGAAGTGTACCC
CGTCAGAAACAACTCCAGATTATGTGAAGTGTGAATGGACATAATTCTACAGTGGAGATAATATAACATAACA
GAAGATGATGTAATACAAAGTCAAAATGCACTGGGAAATATAACACCCAGCATGGCTCTTGTGAATCCAATTCA
TTGAAAAGACTATACTTGAATCACCATTATGTTGGAACCAAACCTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGGTTCTGATACCTGAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCAGAGTGAACACTTGTAAAGGTGTATCCCTTATTGGACACTATGGAGA
TTCCAGTTAATGCCCTAAATTCTTGAGAAGTATGAGCTCTGTGATCTGCAGTGAAAGTTGATATGTGAT
AGCAGTGACCAACCACTCGCTGCAATCAAGGTTGTGCTCCAGAACGAAACGAGACATTCTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTCTGAAAAGGGATCGAAGTGCAGTGGCAATTAGGATTTCAGCAT
GAAACACATGCGGAAGAAACTCCAAACCAGCCTTCAACAGTGTGCATCTGTTCTCATGGTTCTAGCTCTG
AATGTGGTGAATGTAGCGACAATCACAGTGAGGATTGTAAATCAACGGGCAGACTACAAATACAGAGCTG
CAGAACTATTAACTAACAGGCTCAACCCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCCTGAAAGTGAACACACAGGCCATGTAAAAAAAA

FIGURE 70

MELVRLMPLTLLLISCLAEELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPEINCTWTI
ERPENKSIRIIIFSYVQLDPDGSESENIVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTEFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSIIGPIRLKDRSASGNQFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCGGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGCCCTGCCCG
GGACATGCGGCCCGAGGAGCTCCCCAGGCTCGCGTTCCCGTGTGCTGTTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCACAGCGCTTCGACCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCCTCGTGCCAGCTCGTAGCGAGTGGTCTGGTGGTATTGGAAAAGGAAA
AGATAACCGAAGTATGTGAAATTATGAAAGATAATTACCCCTAGTTCAAATATGAAGAT
TTTGGACCACATTACAGAAAATTTTAATGCCAACAGTGGCAGATAAATTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTACCTGTGGGGT
CAGAATATTCTGGAACGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCCCTTGACTGTACTATTCCCTTTGA
ATGGTTTCATCCGCTCTCCTGAGGATGAATCCAGTTCAATTCCATAAGCGGAATTTCAG
TTTCTAAGACATTGCCAGAGCTCATGAGTTAGTGAACAACATACGCCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTCTGGCCTGGTT
ATATAATGAAAGCCCAGTCGGGCACAGTAGTCACCAATGATGTCAGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTCTATAACCTGCAGTGATCGTTATAACCCAGGACATCTTGC
CATAAATGGAAAACATGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG
GAGGAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAGTCAATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCATGCCATTCTAAATGGGCCACATCAGGACAGCTGTCCTGGCCAT
CCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGCCATGGACAGCCACTTAAC
GATTTCTTGGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
CGTGTAAATGGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATTCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACACTGGATAAGAAAATTATTGGCAGTTGCCCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGGGTATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTCTGGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATAACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAATGGTGACCTGTATAGGGCACTTACCAAGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCATTATAAACATAAGTGTACTGTAACCTTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFIHWG
VFSVPSFGSEFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVNTDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPLTLDGTISVVFEERLRQVGWSLKVNGEAIYETYI
WRSQNNDTVTPDVWYTTSKPKEKLVVAIFLKWPMSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCACTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCATCTGGACCACAGGCTCCTGGTCAAGGCTCTTGCCTGCAGAAGAGCT
TTCCATCCAGGTGTATGCAGAATTATGGGGATCACCCTGTGAGCAAAAAGGCGAACCGC
AGCTGAATTCACAGAACAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACATTCAGCTATGGCTGGGTTGGAGA
TGGATTCGTGGCATCTCTAGGATTAGCCAAACCCAAGTGTGGAAAAATGGGTGGGTG
TCCTGATTGGAAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAACCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAGAACATTATTGTCACTGACAGTACCTACTCGGTGGCATCCCC
ACTCTACAATACTGCCCTACTACTACTCCTCTGCTCCAGCTTCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAACAGTTTATGGAAACTAGCACCATGTCACAGAAC
TGAACCATTGTTGAAATAAACAGCAGCTCAAGAACATGAGCTGCTGGGTTGGAGGTG
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGAGCTGGCTTGGATTG
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTACAAACAAAGAACATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCATAAGGAAATCAAAGA
AAACTGATAAAAACCCAGAACAGACTCCAAGAGTCCAAGAGTCCAAGAACACTACCGTGC
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCCTAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAACAGTCCACCC
GGTTCTTAACCTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAAC
CCTTCTCCTATTGTAACCCCTGCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGG
TTCTAGCCTGGCTATGCTCTAAATAATATCCCACGGAGAAAGGAGTTTGCAAAAGTGC
GGACCTAAACATCTCATCAGTATCCAGTGTTAAAAGGCCCTCTGGCTGTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAACACGTATCCCACCTGACATGCTCTTGAGCCGGTA
AGAGCAAAGAACAGGAGAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAATAAGAACATAGAACAGGCTGAGGATAACGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGCAAGTGTCTCTGAAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAAATTCTATTGTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTCTCA
GTTTGATATTCTAGCTTATCTACTTCAAACATAATTCTTATTGCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTATAACACACACAAAG
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGTGCCATTAACAAATGTATCACTA
GCCCTCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA
AGCATTTAGAAAACCTT

FIGURE 74

MARCFSLVLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNSPKCGKNGVGVLIWKPVSQF
AAWCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVSPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASFNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSP
SKTTVRCLAEAV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCGCTCTGCCACGGCTGCCACCCAACGCGAACGAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGAAGAACCGCAGA
TCCATCACTGTGGAGAACATATAGGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACCTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTGCCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGAAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACCAAGTGTCA
TGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCTGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGAAATTGTCAG
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCAACTGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTCAAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCACCCCAAGGACTCTGCTCCCTTAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACCTTGTGCTAGTCCTAAGGAGAACCTTAACCACAAAG
TTTTATCATTGAAGACAATATTGAACAAACCCCTATTTGTGGGGATTGAGAAGGGTGAA
TAGAGGCTTGAGACTTCCTTGTGTGGTAGGACTGGAGGAGAAATCCCCTGGACTTCAC
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSPRLSRWLAQPYYLLSALLSAFLLVRKLPPCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG
GGGCCCCAGCCTGGCCGGGTCAACCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCC
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCACTGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGCTTTCTTACAGTCCCCCA
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG
GTGGCCTCCTTGAGCAGCTCTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCAGCTACGGCCCCGCCACGCCGCCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTTTGCCGCCTGGAAGTTCCATGGCCTGGACCGCTGCCACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCGTGGTTACCCGATCCTAACTGTGGCCCCCAGAGCCTGGGCT
CCGAAGCTTGCTTCCCCGACCCGAGAGCCGTTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCGCCGATTCCTCACTGGCTGTGTATTATTGAGTGGTT
CGTTTCCCTGTGGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCCAAATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGGCATTGCGGTTTGTGGCTTCTG
GAGGGTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCTGGCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGATGGTGGGACAGTTCTCCCTGCC
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAAACTCCCTCCCCGTTCC
TCCCTCTCGGTCAAAGAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCCGCCAA
AAA
AAA

FIGURE 78

MGLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDRDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCCAGCCCCGG
GCGGCAGGGCGCGGGTGCAGAGGGATCCCTGACGCCTCTGTCCTGTTCTTGTCGCTCCCAG
CCTGTCGTCGTCGTTGGCGCCCCCGCTCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCCGCCAGGGCGCTCCCAGACCTAGAGGGCGCTGCCCTGGAGCAG
CGGGTCGTCTGTCCTCTCCCTGCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCCGCCGGCTCCCGCACCCCTGCCCTGCCGCATTCTCCCTCTCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGCTCTGCCCTCGGTGTG
TGTCTGCTGCTGCCGGGCCGCGGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG
TTTACACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTATGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCCCTCAGTAGATGCCATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTCACAGTAACTAAAGGAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGTAAACGACTAAAGAAAACACCCGAGAAGAAAATGG
CAATAAAGATTGTAACAGACAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGGCAGC
GCCGATTTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGGAAATTGGAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTAACTTGAA
AAACTTACATCAGCCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA
ATTCCAATACAGGAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT
CGGAATAATGGCTTCTTCTTACACATGCCAACTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAAGAACCTGTTATAACT
CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCCTC
ATGCTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGTCTAGCTGTATCAGAAACATCCGCTATATGAGTGGTGAACAGCTACTGGT
GATGCCATTCTTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCTTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCAGGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTCTAAACCGAAGGAGTCTCACGCTTCTCACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAA
ATGGTAACATTGACAACAGAAAGAAAAAGTACAAGGGATCCAGTGTAAATTGTATT
CTCATAACTGAAATGCTTACTGATCAGATACTAGAACATACAAAATATTAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCAACCAGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAA

FIGURE 82

MSAAWI PALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSDDIEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVITDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCCGACCCGCGGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC
GGCGGCCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGCGGCTGCGGGCGCAGAGCGGAGATGCCAGCGGCTGGGCCACCCTGCTGTGCCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGGCCGCTCCGACGGCAGCTCGGCTCCAGTC
AAGCCCGCCCGCTCTCAGCTACCGCAGGAGGAGGCCACCTCAATGAGATGTTCCCGGA
GGTGAGGAAGTGTGAGGACACGCAGCACAAATTGCGCAGCGGGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT
ACAATGAGACCAACACAGACAGAAGGGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTGCCAGCTCCAGTACACCTGCCAGGCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCATGACCCGCCAGCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGAGCCGATGCCAGAACAGATGGGAGATCCTGCTGC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGGAGCTGACTGAAGAGATGGCCTGGGAGGCTGCGCTGCCGCT
GCACTGCTGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCAGGTGTGCTTCTGGCTGGCTGACCAGGCTTCCCTACA
TCTTCTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTGCTTCAGC
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCCTGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCAGATTATTGGCTGCTTGCCTCTACCAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG
AGTCTCCCTCTGATTGGTTGGAAATGTGGAGAAGAGTGCCCTGCTTGCAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACGCACTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAAGATGTTCTGTCACCCCTGCATTACATGTGTTATTCTAC
AGCAGTGTGCTCAGCTTACCTCTGTCAGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGAGGGGTATTGTTCTCCTCGTCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCAT
CTGGTTGTGACTCTAACGCTCAGTGCTCTCCACTACCCACACCCAGCCTGGTGCACCAA
AAAGTGTCCCCAAAAGGAAGGAGAATGGGATTTCTGAGGCATGCACATCTGAATTAAG
GTCAAACTAATTCTCACATCCCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCGTCTTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAATGAAATTGCAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTCTCACAGAGTTCTAAAGTTAAAGTTGCACTGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC
ATAAAACTCACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDQ
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVTISVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCQAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCACCTCCACTCTCTCCCTCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTCCCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGACAC
TAAAGCCTTAAGGACAGGCCATTACCTCTGAGCTCCTTGCTTGAGTCAGGAAACATGGGAGGG
CCAGGCACGGTGAACACTGTAACTCCAGCATTTGGAGACCAGGTGAGCAGATCACTGAGGTCAAGG
TTCGAGACCAGCCTGGCAACATGGAGAAACCCCCATCTACTAAAATACAAAATTAGCCAGGAGTGGTGGC
AGGTGCCTGTAATCCAGCTACTCAGGGCTGAGCCAGGAGAATCGCTGAATCCAGGAGGCGGAGGATGCAGT
CAGCTGAGTGCACCGCTGACTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
GGGGTAGATACTGCTCTGCAACCTCTTAACCTGCATCCTCTTCTCAGGGCTGCCCTGATGGGGCCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGGAGGGCAAGAAGTGA
GACGCCG
GTGAGAATGACTGCCCTGGGAGGGTGGTCCCTGGCCCTGGCAGGGTGTGACCCCTACCTGCAAACACACA
AAGAGCAGGACTCAGACTCCTTGTAATGGTCCCTGCCCTGCAGCTCCACCATGAGGCTCTCGTGGCC
ACTCTTGCTAGCTGGGTGGCTGGCACTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCC
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTGCTTACCGCGAGGCTACCAACTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCCTGCTCCTGCAGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCAGGAGAACAGCTTTCGGA
TGCCCGAGACTGTGATTTCATGCCCTGCCAGCTGCTGAGCCTGCACCTAGAGGAGAACAGCTGACCCGGCT
GGAGGACACAGCTTGCAAGGCTGGCAGCCTACAGGAACACTATCTAACCAACCAACAGCTTACCGCATCGC
CCCCAGGGCTTTCTGGCTCAGCAACTTGCTGGGCTGCACCTCAACTCCAACCTCCTGAGGGCATTGACAG
CCGCTGGTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGGGCAACAAAGGTAGATGCCATCCTGGACAT
GAACCTCCGGCCCTGGCCAACCTGCTAGCCTGGCTAGCAGGAGTGGAGACCTGTCAGGAGAACAGCT
CCTGGAGGGCTGCAAAGGCTGGAGAGGCTCTCCTTCTATGAAACACAGCTGGGGGGTGGCCAGGGGGACT
GGAACAGGTGGCCCTCAAGTCCCTAGACCTCAACAAGAACCCGCTCAGGGCTAGGGCCGGAGATCTCC
CAACATGCTGACCTTAAGGAGCTGGACTGAACAAACATGGAGGAGCTGGTCTCCATGACAAGTTGCC
GAACCTCCCCGAGCTGACCAAGCTGGACATCCAATAACCAACCGCTGTCCTCATCCACCCCGCGC
CCACCTGCCCAAGATGGAGACCCCTCATGCTCAACAAACAGCTCAGTCCTGCACCAGCAGCGTGGAGTC
CCTGCCAACCTGCAAGGAGGTAGGTCTCACGGCAACCCATCCGCTGTGACTGTGTCATCCGCTGGGCA
CACGGCACCCTGTCGCTCATCGAGCCGAATCCACCCCTGTGTCGGGAGGCTCCAGCAGCCTCC
GGTCCGTAGGTGCCCTCCGGGAGATGACGGACACTGTTGCCCTCATCTCCCCAGAAGCT
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGGGGCAACCGAACCCGAGATCTACTG
GGTCACTCCAGTGGGCTTCGACTGACACCTGCCATGCAGGCAGGAGGTACCGGGTGTACCCGAGGGAC
GGAGCTGGGAGGGTGACAGCAGAAGAGGCAAGGGTATAACACTGTGTCGGCCAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTGGTTGTGGCGTGCTCTCCAGCCAGGGAGAAGGACAGGGCTGGAGCTCC
GGTGCAGGAGACCCACCCCTATCACATCTGTATCTTGGGTCAACCAACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCGCTGCCCTGGGAACCCACAGCTA
CAACATTACCGCCCTCCTCAGGCCACGGAGTACTGGGCTGCTGCAAGTGGCCTTGCTGATGCCACACCC
GTTGGCTTGTGTATGGGCCAGGACCAAAAGAGGCCACTTCTGCAAGAGCCTTACGGGATCGTCC
TGCCATCTGGCTCTGCTGTCCCTCTGGCAGCTGGGCTAGCGGCCACCTGGCAGAGGAA
GGGTGTGGGTGGAGGGGGCTCTGGCCTGGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGAC
GTCTGCTCCCCCTCGTCCCTGGCCTGGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGAC
ACCATTGTCTCAAAATTCTTGAAGCTCAGCTGTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTAC
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAGGGACATGGACCCACGTGCTTGAGGCTGGCAG
CAAGACAGATGGGGTTGTGGCCCTGGGGGTGCTCTGCAAGCCTTACCTGGCTAGAGCCTCTGCC
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCTGCC
CTCTCTGCCAGAGGCTCCTGGGCTGGCTGGCTGCCCCACCTGTGTC
TCTTCTCTGTACAGTCTCAGITGCTTGCTTGTGCTCTGGCAAGGGCTGAAGGAGGCCACTCC
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGAAGGACATTTGGAGAGGGATGCC
CGCCTCATCTCAGCAGCCTGGGCTGGCATTCCGAAGCTGACTTCTATAGGCA
ATGTGTACACCTCCCCAACCGATTCACTTTCTCTGTAAAAAATAAAATAACAATA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLQLQSNSIVRVDQSELGYLANLTLDLSQNSFSDARCDFHALPQLLHLH
EENQLTRLEDHSFAGLASLQEYLHNHNLQYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMMFRPLANLRSVLVLAGMNLRREISDYALEGLQSLSFYDNO
LARVPRALEQVPGLKFLDLNKPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHLPQMELMLNNNALSAHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPFDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADETKTVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLOVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLA AHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCGCTTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGGGGACATTGTGTACCGCCT
CTACATCGCGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGGCCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGGCCACACTCTCAAGATCCTGGCGTCCTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACCGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAAGGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCTTCATGCTGCACCTCATGACCAATACGACCCGCTACTCCAA
GGCCTTCGGCGTCTCTGTGGAGGTGAGTGAAGAACAGCTGCCGAGCTGAACCTCAACAAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGTGGCCT
CCCTGAGACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCGACGTGACCATCCGCC
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTTCTACACAGCGCCAAAGATTGAAGGCCCTGCGCT
GGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGGGAGAACACCGCTACATGTCATCGA
CGGGCTGGGAGCTCAAACGCTCAAGGTGCTGCCGCTCAAGAGCAACCTAACGCAAGCTGCCACAGGTGGTCAC
AGATGTGGCGTGCACCTGCAAGACTGTCCATCAACAATGAGGGACCAAGCTCATGTCCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTCAGCCT
CCACAACTGCAAGGAGATTGACCTCAAGGACAACACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCCTCACCTGCTTAAGCTGTGTTACAACCACATGCCCTACATCCCCATCCAGATCGGCAACCTCACCA
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGAAGATCCCCACCCAGCTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCTCCCTGCCGACATGCCCTCTGCAGAACCTCCAGAACCT
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCAGGAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCAGTCCAGGGTGGCGAGCTGACCAACCTGACGCAAGATCGAGCTGCCGG
CAACCGCTGGAGTGCTGCTGTGGAGCTGGAGCTGCCACTGCTCAAGCGCAGCGGCTTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAG
GCCGGCCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCCGGAGCTTCCAGGCCGGAGGGCAGGCCTAGCTTCTCCAG
AACTCCGGACAGCCAGGACAGCCTCGGGCTGGCAGGAGCCTGGGGCGCTTGTGAGTCAAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGTGTTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCTCCCTGGAGGGCAGCTCTGCCCAAGGGCTGAG
CTGCCACCGAGGTCCTGGGACCCCTACTTAGTTCTGGTATTATTTCTCCATCTCCACCTCCTTCATCC
AGATAACTTATACATTCCCAAGAAAGTTCAAGGAGCTTCAAGGAAAGGTGTTAGGGAAAGGTGGCTGCC
TTGTCCCTATTAGCGATGCCCGGGCATTTAACACCCACTGGACTTCAGCAGAGTGGTCCAGGGCAAC
CCATGGGACGGTCACCCAGCAGTGCCTGGCTCTGCCGTTCCACGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGCTGGAGCTGCCCTTCAGTTTGTTGAGTTAGTTTTGTTTTTTAACTAAA
AAACAATTTTTAAAAAAAGTTGAAATGGATGGTTGGGTATTAAAAAGAAAAAAACTAAAAAAA
AAAAGACACTAACGCCAGTGAAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGCCAGACGT
TGAACACTGTGTTCCCTTCCCTGGCGCAGGGTGCAGGGTCTTCCGGATCTGGTGTACCTGGTCCAGGAGTT
CTATTGTTCTGGGAGGGAGGTTTTGTTGTTGGTTTTGGTGTCTTGTGTTCTTCTCC
ATGTGCTTGGCAGGCACTCATTTCTGTGGCTGCGCCAGAGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGATGAACGGTGTCCATTGCACTCCCTCCTGCGCTGCCCTGCCTCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTGCCTCAGACTTGTGTTCCCCACCTCTGCCATGGGTGT
CCAGTGCACCGCTGGCTCCGCTGCTCCATGCCCTGCGCACCTGGCTCTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGTGCGCCCTGGGAGGGCAGGCCGTTGGTCCAAGGCCGTTCCCTGGCGC
CTGGAGTGACACAGCCAGTGCCTGGCAGCTGGTGGCTGGAAGCCAACCTGCTTGTAGATCAACTGGTCCCCACCTT
AGAAGGGTCCCCGCCCTAGATCAATCAGTGGACACTAAGGCACGTTTAGAGTCTCTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCATTGTTCTGCGTCGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIKVIKFILIIICYTVYYVHNIFDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLSGLPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNQEIIDLKDNNLKTIEEISFO
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVLQSLPSRVGELETNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCGT
CCCGCGGTGGTTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCCTGGGCACTGGGTTCAAGTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGAACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGCGGGGGT
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTTCGAAGACAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGGCCACCTAGTTGTCTTGTCAAGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGGCCAGTCATTGCAAGCTGGATCTCGTAGATAACCATGGTCAGGAGGCCTG
AACGTGACGGTGTATAATGGACAGCTGGATCTCGTAGATAACCATGGTCAGGAGGCCTG
GGTGGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTCCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAETCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTAAAAAAACCTAACAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLIAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVILNAVNKGLYRE
ATELGKAEMIIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTAGTGATCCCTCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCAGTGCATCTCCCCACACCCTCAGGAAGTTCAAGGTGCCATCATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGAAGGATGCCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGCCCAATCGGCCGGTGTACACCAATATCAGCCACCACTTGAGTGGATCCAGAACAG
CTGATGGCCAGAGTGGCATGTCCCAGGCCAGACCCCTCCTGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDALP
SPHTLQEJVQVAINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACCGCGTCCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGCCCTGGGCCGTGGGACCCCTGAGGAAGAGCTGAGTCACCTT
GCCCTGAGACAGCAGAAATGTGAAAAGACTCTCGGAGCTGGTGCAGGCTGTGCGGATCCCAG
CTCTCCTCAATACGAAAATACCTGACCCTAGAGAAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCCTCACACGGTGCAAAATGGCTCTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATTGACAAGCAGAGCTGCTGCTCCC
TGGGCTGAGTTCATCACTATGTGGAGGACCTACGGAAACCCATTTGTAAGGTCCCCAC
ATCCCTACCAGCTCCACAGGCCCTGGCCCCCATGTGGACTTGTGGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCCTGTGATCGTAAGCGATAACACTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTCTCGGTGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCGGGCGGGCGGGATTGAGGCCAGTCTAGATGTGAGT
ACCTGATGAGTGTGGCCAACATCTCACCTGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT
GGGGCGGGTGTGGCTGTCTGGAAAGACACCAGTTCCGCCTACCTTCCCTGCCCTCCAG
CCCCTATGTCACCACAGTGGAGGCACATCCTCAGGAACCTTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACCTGCCACCATTCCAGTTACTCAATGC
CAGTGGCGTGCCTACCCAGATGTGGCTGCACCTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCTATTCCATGGGTGTCGGAACCTCGGCCTCTACTCCAGTGGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGCCTGTC
TGGATGAAGAGGTAGAGGGCAGGGTTCTGCTCTGGCTGGATCCTGTAACAGGC
TGGGAACACCAACTTCCAGCTTGTGAAAGACTCTACTCAACCCCTGACCCCTTCTATC
AGGAGAGATGGCTTGTCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCTGAAA
TGCTGTGAGCTTGACTTGAACCTCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTGGATGCTCTCCCTCCGC
ATCTCATCTTCTCTTCACTCAGGCTTCAAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATTTGCTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTCTG
ACTACTCTGTCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCCATTGTAGATTTGCTCTCAGTTACTCATTGTCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVALVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAARGLTLLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCCCAGGCCACACCTGTCTGAGCGGCAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTG
GCCTGCATAACCGCCTCCCTGTCGTCTGGCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTAAGGAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTCAGGAAAGTCTCGAAGGAAGCAGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAAAGGACTTCCTGCTCAACTACCCTTCTAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA
TACACGATGGAAAACCTATGTGAAAGGAACCCAGAACAGCTCGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACCTAAAGCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGCCAGCGGGTCTGGGTCTAT
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACAGCAATGCGATGCCAGCCAGGGGCCAGCGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACAGTGGAGCGAAAAATTATTGGCATTTCAGG
GCACCAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGGCCCTCTGGCAGCAATTAGGGCTTCTGTGTTCTTATTAGGAGAGGCC
AAATTGTTTTGTCATTGGCGTGCACACGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAGTTAATCTTCACGTTTG
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATATTGACATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVL
TAACIHDGKTYVK
TQKLRVGFLKPDKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKG
WIKGANDIGMDYDYA
LLELKPKPHRKFMKIGVSPPAKQLPGGRIHFGYDNDRPGNLVYRFCDV
KDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNV
AVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCTGAGCCTGCTGCCGTCCCCCCCCACCAGCCATGGTGGTT
CTGGAGCGCCCCCAGCCCTGGTGGGGCTGTCTGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTTGCTCACAGCCGTGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTCGCTGGTGGAGC
CCCACCTGTGATTCTGGAAAGGAAGGTGCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATTCAAGATGGAGTTCCCTTG
CCCACCCCTCAGACCCTGCAGAACGCTGAAGGTTCCATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCTGGTGGAGAACATCGTCAAGGGTGCA
GCTCCGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCGGCGGCTCTAGGGCGCAGCGGACGCCGCTCGGATCTGAAAGGCGGCAGATCCACA
TCTGGATCTGGATCTGCAGGGCGCTCGGGCGTTCCCCCGCTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCGGACGGCTGCTCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCAC
GACTTCCGGCCCCGCCCGGGCCCGAGCGCTTTGTGTATATAATGTTAATGATTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTATTCTCCAATTCAATAATTATTATT
CTCCAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFSTSLLLASTAILNAARI PVPPACGKPQQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLF SVLLGAWQLGNPGSRQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDA CLGDSGGPLMC
QVDGAWLLAGII SWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGCCCTCACAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGGGCGCCGGCGAGAATCTGTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGCCATGGAGGAGTGGCACCACGAGCGTAGCAGTACAAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCAAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCTACCTGGTAAGTGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGGCCAGAGAACTCTCTGGACCCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGAGCTGAGGCTGAGTTGCCTCCTCAGTG
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGCTTGGCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTCAAGGCTGAACCTGGGCCCTGGTCAATGTGTGGGCCCTCTGGGA
CTACTGCTCCTGCCTCTGGTGTGGCTGGAAATCTTCTGAATGGATAACCAACTCAAAGGG
TGAAGAGGTCAAGCTGTCCTCTGTCACTTCCCCACCCCTGTCCCCAGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCACCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGTGGAGGATTGAGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC
TTTGAGTGGGGAGGCAGGGACGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLRYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVDPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTAEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPPVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACCTGAAAGTCAGGCTTTCATTTGGGAAGCCCCCTAACAGAACCGTCAATTCTCCAAGTTATGGTGACGT
ACTTCTGTTCTCCCTCTGCTTGTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTCAT
CAAGGCAGATTCCATGAGCCACCTTCAAAGCCTCGAGAAGTGAAGACTGAACAAACAATGAATTGGAGACCATTCC
AAATCTGGGACCAGTCTCGGAAATATTACACTTCTCCTTGGCTGGAAACAGGATTGTGAAATACTCCCTGA
ACATCTGAAAGAGTTCAAGTCCCTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATT
TCCAGCCTACAGCTAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAA
TTTGGCAACACACTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACT
GCCCAACTGCAACATCTCGAATTGAACCGAAACAAGATTAAGATGGAGTGAATTCCAAAGGCTTGG
TGCTCTGAAAGTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAA
CATGGAAATTGAGCTGGAGCCTAACAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTTCATCTCAGCCAAATGCCATCAACAGGATCAGCCTGATGGCTGGAGTCTGCCAGAAGCTCAG
TGAGCTGGACCTAATTCACTTCACTTCAAGGTTAGATGATTCAAGCTTCCCTGGCCTAACGTTACTAAATAC
ACTGCACATTGGGAAACAAGACTCAGCTACATTGCTGATTGTGCTTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAGAACAAATGAAATTCTCTGGACTATTGAAGACATGAATGGTGTCTTCTGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTCTTACAAGGAATGCATTTCACAAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGGTGGCGAAAACAACCT
TCAGAGCTTGTAAATGCCAGTTGTGCCCCATCCTCAGCTGCTAAAAGGAAGAACGATTGGTGTAGCCAGA
TGGCTTGTGTGATGATTCCCAAACCCAGATCACGGTCAGCCAGAACACAGTCGGCAATAAAAGGTT
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTGCTTGGAAAAAAAGAACATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCAACGGTGGCAGGTGATGGAGTATACCAC
CATCCTCGGCTGGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGATCTCCAATCACTTGGTTC
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACC
CCGAGCTGGGCCATGGCACGCTTGGAGTGTGCTGTGGCACCCAGCCCCCAGATAGCCTGGCAGAAC
TGGGGCACAGACTCCAGTGCACGGAGAGACGCATGCATGTGATGCCGAGGATGACGTGTTCTTATCGT
GGATGTGAAGATAAGGGACATTGGGTATAACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCA
AACTCTGACTGTCTAGAAACACCATCATTTCGGGCCACTGTTGGACCGAAGTGTAAACCAAGGGAGAACAGC
CGTCCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAAACTGGACCAAAGATGATGCCATTGGT
AACCGAGAGGCACTTTTGAGCAGGAACTCAGTGTGATTATGTTGACTCAGATGTCAGTGTGATCCCCACTCA
ATACACATGTGAGATGTCTAACACCCCTGGCACTGAGAGAGAACAGTGCCTCAGTGTGATCCCCACTCA
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTAGACGATGACGGATGGCCACTGTGGTGTGATCATAGC
CGTGGTTGCTGTGGTGGCACGTCACTCGTGTGGTGGTCACTGATCATATACCACACAAGGGGAGGAATGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTCTAGTTATTGTGATCTCAGGGAA
AGCTGACAGGCAGGATGGTACGTGTCTCAGAAAGTGGAACGCCACCAAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACCAACATGACAGTAGTGGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC
CACAGATCTTCTTGTCCGTTTGGATCCACAGGCCATTGATTTGAAGGGAAATGTGTATGGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAAGAACAGTTTAATGGACCACTATGAGCC
CATAAAGAAAAGGAGTGTCTACCCATGTTCTCATCTTCAGAAGAACCTGCGAACGGAGCTCAGTAATATAC
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGGACCTGGAAATGAAA
TCTAAACAAGTCCTCTTAGATTAGTGCACAAATCCAGAGCAGCGTGGTGCCTCGAGTAATTCTT
TACCTTGAAAAGCTCTCAGGAGACCTCACCTAGATGCTTACTCAAGCTTGGACAGGCCATTGTCAGCC
AAGAGCCTTTATTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGTCAAGAGGAAGATGGGAAAGAAC
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGACTCAGAACATTTCAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACACTACCTCAAGTGAACTTT
AAAGAGAGAGAAATCTTATGTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGAT
GAACCAAAATTACAAAAAGTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAACAC
TTTTTTAACTTTGTTTATGCAAAAAGTATCTTACGTAAAATTATGATATAAACATGATTATTTATGTATT
TTATAATGCCAGATTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCC
TTAAATAGAAGTTACTTCATTATATTGACACATTATTTAATAAAATGTGTCAATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRSLFIKASSMSHLQLSLREVKLNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASAIPPKMFKLPQLOHLELRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHLRSRLLDDSSFLGLSLLNTLHIGNRVSYIADCAFRLSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPQWVAEENNQSFVNASCAPOLLKGRSIFAVSPDGVC
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSC
SAGSISANATLTVLETPSFLRPLLRTVTKGETAVLQCIAGGSPPP
KLNWTKDDSP
LVTER
HFFAAGNQLLIIVDSDVSDAGKYTC
EMSNTLGTERGNVRLSVIPTPTCDSPQM
TAPS
LDDDG
WATVGVI
IAVVCCVVG
TSLVWVII
YHTRR
RNEDCS
ITNTDETNLPAD
I
PSYLSSQGT
LAD
RQDG
YVSSES
GGSHHQ
FVTSS
GAGFFLPQHDSS
GTCHIDNS
SEAD
VEA
ATD
LFLCP
FLGSTGP
MYLKGNVY
GSDPF
ETYHTGC
SPDP
RTV
LMDHY
EPSY
IKK
KEC
YPC
SHP
SEES
CERS
FSN
NISW
PSHVR
KLLNT
SYSH
NEGPG
MKNL
CLNK
SSLD
FSAN
PEP
ASV
ASS
NSFM
GTFG
KALRR
PHLDA
YSSFG
QPSDC
QPR
AFYL
KAHSS
SPD
LDS
GSEED
GKERT
DFQE
ENH
ICTF
KQT
LEN
YRTP
NFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTGGTGGTGGCTGTTGGTGCCTTGCAAAAATG
AAGGATGCAGGACGCAGCTTCCTCGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTTGTGAGCCCTGGATCTTAACACAAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGGGGTTGGTGTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAAGAACCGAGGATTCAAAGAAAAAGTATGTTCATTTTCTC
TATAAGGAGAAAGGAGATTTTGAATTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGAAAGAAA
GGTGTGGTGGTGTCTTCTTGTGAAATTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGAAAGAAA
TTTCAGAGAAGAAAAGTGTACCGCGCAGATTGAGGCATTGATTGGGGAGAGAACCGCAGAGCACAGTGG
TTTGTGCCATGTTGACTAAATTGACGGATAATTGCAAGTGGATTTCATCAACCTCCTTTTAAAT
TTTATTCTTTGGTATCAAGATCATGCGTTCTTGTCTTAACCACTGGATTTCATCTGGATGTTGCT
GTGATCAGTCTGAATAACACTGTTGAATTCCAAGGACCAACACAGATAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGTCCTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGC
GCTGGCTCTCAACTCTGGTGGCTGGTCTGGTGCAGACCTGCCCTCTGTGTGCTCCTGAGCAA
CCAGTTCAGCAAGGTGATTGTGCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCACCAACACACGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGCACCTGGAAATCCT
ACAGTTGAGTAGGAACCATACTAGAACCATTGAATTGGGGCTTCAATGGTCTGGCAACCTAACACTCTGGA
ACTCTTGACAATCGTCTTACCATCCGAATGGAGCTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT
GCGAAACAACCCATTGAAAGCATCCCTCTTATGCTTTAACAGAACTCCTCTTGCGCCGACTAGACTAG
GGAATTGAAAAGACTTCATACATCTCAGAAGGTGCCTTGAAAGGTCTGTCCAATTGAGGTATTGAAACCTTG
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTCTGGAAATCA
TTTATCTGCCATCAGGCGTCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACAGTCCCAGAT
TCAAGTGAATTGAAACGGAATGCCCTTGACAACCTCAGTCACTAGTGGAGATCAACCTGGCACACAATCTAAC
ATTACTGCCTCATGACCTCTCACTCCCTGCACTCATCTAGAGCGGATACTTACATCACAAACCCCTGGAACTG
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACAGCAGCTTGTGCCCCGGTG
TAACACTCCCTCCAACTTAAAGGGAGGTACATTGGAGAGCTCGAACAGAACATTACTTCACATGCTATGCTCCGGT
GATTGGGAGCCCCCTGCAGACCTCAATGCACTGAAGGCATGGCAGCTGAGCTGAAATGTGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGCGTACAAAGTGGGATAGCTGT
GCTCAGTGTGGTACGTTAAATTCCAAATGTAACTGTGCAAGATAAGGCATGTACACATGTATGGTGGTAA
TTCCGGTGGGAAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCACACTCCTTCTTACTTT
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACACAGATAACAATGTGGGCCCCACTCC
AGTGGTCAGTGGGAGACCACCAATGTGACCACTCTCACACCACAGGACACAAGTCGACAGAGAAAACCTT
CACCATCCCAGTGACTIONATAAACAGTGGGATCCAGGAATTGATGAGGTCTGAAGAGACTACCAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGTGCTGGTCAATTCTACAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCAACAAGGACTGTTGAAATTATAATGTGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCCTGCTATGAGCATGAGCACCTAAACTACATACAAATCTCCCT
CAACCAACACAACAGTTAACACAATAAATTCAATACACAGTCAGTCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACATCAAAAAAA
GACAGTTTATTAAGGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTTATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIVNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDDELDSGNHLSAIRPGSFQGLMHQKL
WMIQSQIQVIERNADNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWNCNC
WLSWWIKDMAPSNTACCACRNTPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN
TTASATLNVTAAATTTFPSYFSTVTVETMEPSQDEARTTDNNVGPTVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDIEITGDTPMESHLPMMPAIEHEHLNHYN SYKSPFNHTTVNTINSIHSS
VHEPLLIRMN SKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCCTTCCGTTCTGCTGTTGGGGCA
TGAAAGGGCTTCGCCCGCGGAGTAAAAGAAGGAATTGACCGGGCAGCGAGGGAGGAGCGCAGCGACCGC
GAGGGCGGGCGTGCACCCCTCGCTGGAAGTTGTGCGGGGCCCGAGCGCGCAGGGCTGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCCGCGGGGTTGGGCTGCTGTC
GCGGTGCTGGGGCGCGTGGGGCGTCCGGACAGCGCGTCCGGGGAACTCGGGCAGCCCCTCTGGGTAGCGCC
GAGCGCCCATGCCCCACTACCTGCCGCTGCCCTGGGACCTGCTGGACTGCGAGTCAGTAAGCGCTAGCGCT
CCCGAGCCACTCCCCTGGCTGGACTTAAGTCACAACAGATTATTCATCAAGGCAAGTCC
ATGAGCCACCTCAAAGCCTTCGAGAACTGAAACTGAACAACAATGAATTGGAGACCATTCAAATCTGGACCA
GTCTCGGCAAATATTACACTCTCCCTGGCTGAAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACTTGGACCTAGCAGCAACAATTTCAGAGCTCAAACAGCATTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGAACTGGGTATTTGACAATTGGCCAACACA
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAGATGTTAAACTGCCCCAAGTCAA
CATCTCGAATTGAAACGAAAACAAGATTAAGATGGACTGACATTCCAAGGCCCTGGCTCTGAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGAAATTGG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGATGCTGCAGGAACCTCAT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCCTGGCTAAGCTTAACATACACTGCACATTGGG
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCAAGTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTGTCTCTGGGCTTGACAAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCAGTGGTTGGATGCAATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATTGCAATTAAATACA
TCAAGGCTTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAACATTCAAGAGCTTGTA
AATGCCAGTTGTGCCCATCTCAGCTGCTAAAAGGAAGAAGCATTGGTGTGCTGCTGCTGCTGCTGCTG
GATGATTTCCCAACCCCCAGATCACGGTTCAAGGCTGGAGAAACACAGTCGCAATAAAAGGTTCCAATTGAGTT
ATCTGCTCAGCTGCCAGCAGCAGTGAATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGAACTACTGCATGAT
GCTGAAATGGAAAATTATGCAACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACACCATCCTCGGCTG
CGCAGGGTGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCAATTGGTCTATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATCAGCAAGACCCCATGGATCTCACCATCGAGCTGGGCC
ATGGCACGCTGGAGTGCTGCTGTGGGCCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC
TTCCAGCTGCACGGAGAGACGCATGCACTGATGGAGCTGGCAGGGATGACGTGTTTATCGTGGATGTGAAGATA
GAGCACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAGTATTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTTCGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGCTCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATAGCCATTGGTGGTAACCGAGAGGCAC
TTTTTGCAGCAGGCAATCAGCTCTGATTATTGGACTCAGATGTCAGTGATGCTGGAAATACACATGTGAG
ATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCAACCTGCGACTCCCCT
CAGATGACAGCCCCATGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCGTGGTTGCTGT
GTGGGGGCCACGTCACTCGTGTGGGTGGTCACTCATATAACACACAAGGGCGAGGAATGAAGATTGCAGCATTACC
AACACAGATGAGACCAACTTGCACAGCAGATATTCTCATGTTATTGTCATCTCAGGGAAACGTTAGCTGACAGGCAG
GATGGTACGTGCTTCAAGAAAGTGGAAAGCCACCCAGTTGTGACATCTCAGGGTGTGGATTTCATACCA
CAACATGACAGTAGTGGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTC
CTTGTGCGTTGGATCCACAGGCCCTATGTTGAAAGGGAAATGTGATGGCTCAGATCCTTGGAAACACA
TATCATACAGGTTGCAGTCCCTGACCCAAGAACAGTTTAATGGACCAACTGAGCCCATGAGCTTACATAAAGAAAAAG
GAGTGCCTACCCATGTTCTCATCCTCAGAAGAATTCTCGAAGCGAGCTTCAGTAATATATCGTGGCCTCACAT
GTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAAATGAAAATCTGTCATAACAAGTCC
TCTTTAGATTTAGTGCACATCCAGAGCCAGCGTGGTTGCCCTCGAGTAATTCTTCACTGGTACCTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCCATGAGCTGAGCCAAAGGCCCTTAT
TTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGTCAAGGAGAGATGGAAAGAAAGGACAGATTTTCAAGGAA
GAAAATCACATTGTACCTTAAACAGACTTAAAGAAAATCAGGACTCCAAATTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGCTTAACATACACTACCTCAAGTGAACCTTTATTAAAGAGAGAAT
CTTATGTTTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGATGAACCAAATTAC
AAAAAGTTATGAAAATTATTAACGGAATGATGCTCATATAAGAATAACCTTTAAACTATTTTAACTTTG
TTTATGAAAAAAAGTATCTACGTAATTATGATATAATCATGATTATTTATGTTATTTATAATGCCAGA
TTCTTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTTAAATAGAAGTT
ACTTCATTATATTTCGACATTATTTAATAAAATGTGCAATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAEARPCPTTCRCLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRNLSFIKASSMSHLQLSREVKLNNNELETIPNLGPV
SANITLLSLAGNRIEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNR
VTSMEPGYFDNLANTLLVLKLNRRNRIASIPPKMFKLQLQHLELRNKIKNVDGLTFQ
QLGALKSLKMQRNGVTKLMGAFWGLSNMELQLDHNNLTEITKGWLGYLLMLQELHLS
SQNAINRISPDAWEFCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNR
VSYIADCAFRLSSLKTLDDLKNNEISWTIEDMNGAFSGLDKLRRLILQGNR
IRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKKLQQLHLNT
SSLLCDCQLKWLPOVVAENFQSFVNASCAPQLLKGRSIFAVSPDG
FVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWK
KDNELLHDAEMENYAHLRAQGGEVMEYTTILRLREVEFASEGKYQC
VI SNHFGSSYSVAKLT
VNMLPSFTKTPMDLTIRAGAMA RLECAAVGH
PAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDV
KIEDIGVY
SCTAQNSA GSISANATLT
VLETPSFLRPLLRTVKGETAVLQCIAGGS
PPP
KLNWT
KDDSP
LVVTERHF
FAAGNQLL
IIVDSDV
SDAGKY
TC
EMSNTL
GTERGN
VRLS
VI
PT
PTC
DSP
QM
TAPS
LDDDGWA
TVGVVII
IAVVCCV
VGTS
LVWVVI
IYHTR
RNEDCS
ITNT
DET
NLP
ADI
PSY
LSS
SQGT
LADRQ
DGYV
SSES
GS
SHQF
V
TSS
GAGF
FLP
QHD
SSGT
CHID
NS
SEAD
VEA
ATD
LFLCP
FLG
STGP
MY
LKGN
V
Y
GSD
PF
ETY
HTG
CSP
DP
RT
VLM
DH
YE
PSY
IKK
KE
C
Y
PC
S
HP
SE
E
SC
RS
FS
NI
SW
PS
HVR
K
L
LNT
SY
SH
NEG
PGM
K
NL
C
LN
K
SS
LDF
SAN
PEP
A
V
S
A
S
NS
FMG
T
FG
K
AL
RR
PH
L
DAYS
SFG
QPS
DC
Q
P
R
A
F
Y
L
KA
H
SS
P
D
L
SG
SE
ED
G
K
ER
T
D
F
Q
E
E
N
H
I
C
T
F
K
Q
T
L
E
N
Y
R
T
P
N
F
Q
S
Y
D
L
D
T
Signal sequence:
amino acids 1-27
Transmembrane domain:
amino acids 808-828
N-glycosylation site.
amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020
Glycosaminoglycan attachment site.
amino acids 886-890
Casein kinase II phosphorylation site.
amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085
Tyrosine kinase phosphorylation site.
amino acids 667-675
N-myristoylation site.
amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939
Leucine zipper pattern.
amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGAGAGCGCCCAGCTTGACTTGAATGAAAGGAGGCCAGGCCGGAGCCGAGCGCAGCTGAGAC
TGGGGAGCGCGTTGGGCCTGTGGGCCTCGCGCCGGCGCAGCAGGGAAAGGGGAAGCTGTGGCTGCC
CTGCTCCACGAGGCCTGACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTATATA
GAAACCTTCCACACTGGAAAGGCAGCGCCGAGGCAGGGCTCATGGTGACCAAGGAGGCCGGCTGATCTGCAG
GCCACAGCATTCCGAGTTAACAGATTTAACAGATAACAAATGAAAGGGAGGAGGCCAGAACAGCTGCCTGGT
TCCATCAGCCCTGGCCAGGCATCTGACTCGGCACCCCCCTGCAGGCCACATGCCAGAGGCCGGGTGCTGC
TGCTCCTGCTGCTGCCAGCTGACCTGGGACCTGTGCTTGCGTGGAGGCCAGGATTGGCG
GTGGCGGCCACAGCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGCCGGTGTGGTACTGAGCCCTGAGG
AGCCCGGGCTGGCCAGCCGGTCAAGCTGCCCGAGACTGTGCTGTCCAGGAGGCCGTGTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCCGGGGACCTGCTGAGCACACCAACCACCTATCTCTGAGAACACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGCTGCACCGGCTGGAGACACTGAACCTGAAACCAACCGCCTGA
CTTCCCAGGGCTCCAGAGAACGGCTTGAACATCTGACCAACCTCAATTACCTGTACTTGGCAATAAACAGC
TGACCTGGCACCCGCTCTGCCAACGCCCCGTATACCTGAGTCAGCTGTGACTTGCTGCCACTATCTCACCAAGATCT
ATGGGCTCACCTTGGCCAGAACGCCAAACTTGAGGTCTGTGACTTGCACAACAAAGCTGGCAGACGCCGGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCTCATCCTGTCCAGCAACTTCTGCCACGTGC
CCAAGCACCTGCCCTGCCCTGTACAAGCTGCACCTCAAGAACAAAGCTGGAGAAGATCCCCCGGGGCC
TCAGCGAGCTGAGCAGCCTGCCAGCTATAACCGTCAACAAACCGCGTGGAGCGCTGCCAGTGGCCTGCTGCCGCGTGC
CCTCTGGAAGCTCCAGCTGGAGTACCTGGATCTGTCCAGCAACAACTGTCTGGTCCAGCTGGCTGC
CGCGCAGCCTGGTGTGCTGCACCTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGTCACAGCAACCAGCTGCCGGAGCAGGCCATCCACCCACTGCCCTTCCAGGGCC
TCAAGCGGTTGACACGGTGCACCTGTACAACACCGCGTGGAGCGCTGCCAGTGGCCTGCTGCCGCGTGC
GCACCCCATGATCCTGCACAACCAGATCACAGGATTGGCGCGAAGACTTGCACCCACTACTTCTGGAGG
AGCTCAACCTCAGTCAACACCGCATACCAGGCCACAGGTGACCGCGACGCCCTCCGCAAGCTGCCCTGCTGC
GCTCGCTGGACCTGTGGGCAACCGGCTGACACAGCTGCCACCTGGGCTGCCATGGCTCAGCTGCGTGAGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCAGCAGGGGGCTGGCGCATGGCTCAGCTGCGTGAGCTGAACCTCA
CCAGCAACCGACTGCCAGGCCAGCCCTGGGCCCCCTGGCTGGGAGCTGCCATCTGAGCTGCTGGACA
TCGCCGGAATCAGTCACAGAGATCCCAGGGCTCCCGAGTCACTTGAGTACCTGTACCTGAGAACAAACA
AGATTAGTGCCTGCCCCCAATGCCTGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAGC
TGGCTGGGCTCCGTGGTGGACAGTGCCTTCCGAGGCTGAAGCACCTGAGGTCTGGACATTGAAGGCAACT
TAGAGTTGGTGAATTCAAGGACCGTGGCCGTTGGGAGGAAAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAACAAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCACTTTCTGC
AGCACACGCCCTGTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCAGCTGCACACATGAGGCA
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTCCCACGGCGTGTCCACGCCAGACACATGC
ACACACATCACACCCCAAACACCCAGCTGCCACACACAACTACCCCTCAAACACCACAGTCTGTACAC
CCCCACTACCGCTGCCAGCCCTCTGAATCATGCAGGGAGGGCTGCCCTGGCACACACAGGCC
TTCCCTCCCCCTGCTGACATGTGATGCGTATGCATACACACCACACACATGCACAGTCATGTGCGA
CAGCCCTCAAAGCTATGCCACAGACAGCTTGCCTGCCAGGCCAGAACATGCCATAGCAGCTGCCGTGTGCC
GTCCATCTGCCGTCCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTGTGGCCAGGTGCCACCCCT
GGAACTCACAAAAGCTGGTTTATTCTTCCATCCTATGGGACAGGAGCCTCAGGACTGCTGGCTGGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTGCCAGGCCCTGGCAGGACA
CAGGCACTTTCCAATGGGAAGGCCAAGGCCAGTGGAGGAGGATGGAGAGGCCCTGGGTGCTGCTGGGGCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGTGCACCTAGGAGAACCTTT
GTTCTCAGGCCTGTGGGGAAGTTCGGGGTGCCTTATTCTTATTCTTAAGGAAAAAAATGATAAAAT
CTCAAAGCTGATTCTTCTGTTAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

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FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSrvlllllPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFEEEEPVVLVLSPEEPGPAAVSCPDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETLNQNRRNLTSGLPEKAFEHLTNLNLYLANNK
LTLaPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLIILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVTPIRSLLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPrrvrtLMILHNQITGIGREDFATTYF
LEELNLSYNRITSQPQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAfdSTPNLKGIflRFNKLAVGSVVDSAfrRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGCGCCCGCAGCAGACCTGCTCCGGCGCGCCTCGCCGCTGTCCCTCCGGAGCGGCAG
CAGTAGCCC GGCGCGAGGGCTGGGGTCTCGAGACTCTCAGAGGGCGCTCCATCGCGCCCACCA
CAACCTGTTCCCTCGCGCCACTCGCGCTCGCCCCAGGACCGCTGCCAACATGGATTTCCTGGCGCTGGT
GCTGGTATCCTCGCTCACCTGCAGGGGGCCGAGTTCGACGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGTCGTTATGGTGGGAGGATGACTGCTGCTGGGCTGGGCTGCCAGTCTGGGACAGTGTCA
TGTGTGCCAACCAGATGCAAACATGGTAATGTATCGGGCAAACAAGTGAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCGCCCTGTAAGCACAGGTGCATGAACACTTA
CGGAGCCTACAAGTGTACTGCTCAACGGATATATGCTATGCCGGATGGTTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACGTCACTATGGCTGTGATGTTGTAAGGACAAATACGGTGCAGTGCCCATCCCCGGCT
GCACCTGGCTCTGATGGGAGGACCTGTGATGTTGATGAATGTCTACAGGAAGAGCCTCTGCCCTAGATT
TAGGCAATGTGTCACACTTTGGGAGCTACATCTGCAAGTGTCTAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTGTCATGACATAGACGAACTGCTACTGGTCAGTATCAGTGCAGCAGCTTGCTGATGTTATAA
CGTACGGGGTCTACAAGTCAAATGTAAGAAGGATACCAAGGGTGTGGACTGACTTGTGTGATATCCAAA
AGTTATGATTGAAACCTCAGGTCCAATTGATACCAAGGGAAATGGTACCAATTAAAGGGTACACAGGAAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCCTATCATTACCAA
CAGGCCCTACTTCTAAGCCAACAAGACCTACACCAAAGCCAACACCAATTCTACTCCACCAACCA
CCTGCCAACAGAGCTCAGAACACCTTACACCTACAACCCAGAAAGCCAACCAACCGGACTGACA
ACTAGCAGCTCCAGTACACCTCCAGGAGGGATTACAGTGTACAGACAGACAGCCCTCAGAAACCCAGAGG
AGATGTGTTAGTGTCTGGTACACAGTGTAAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAAACAACTAGGGACCCAGCAGGTGGACAAATATCTGACAGTGTGGCAGCCAAAGCCCAGG
GGGAAAAGCTGCAGCTGGTGTACCTCTGGCCCTCATGCATTAGGGACCTGTGGCTGTCAATTAGGCA
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACAGCGTGCACGGGAGCAGCCCTGTG
GGGAAGAAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCGAGGGGCTGACATCAAGAGC
AAATCACAAGATGATTAAAGGGTTGGAAAAAAAAGATCTATGATGGAAAATTAAAGGA
ACTGGGATTATTGAGCCTGGAGAAAG
AGAAGACTGAGGGGAAACCAATTGATGTTCTCAAGTATATGAGGGTTGGCAGAGAGGGTGGCAGCTG
TTCTCCATATGCAAGAATAGAACAGAGGAAACTGGCTAGACTAGTATAAGGGACCAATTCTGGCAGG
GGCCATTGTTAGAATACTCTATAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAAAATTAGA
TAAAAATTGTCATTTAAGATGGTTAAAGATGTTCTACCCAAAGGAAAGTAACAAATTATAGAATTCCCAA
AGATTTTGTGTCATGGATGATGTTAGTATGCACTGAAAATCTTACAAGTAAATAATTGGACAAGGCT
ATTAGG
CATTTCCCTTGTGACCTCTAATGGAGAGGGATTGAAAGGGAAAGGCCACCAATGCTGAGCTACTGAAATA
TCTCTCCCTTATGGCAATCTAGCAGTATTAAGAAAAGGAAACTATTATTCCTAAATGAGAGTATGATGGAC
AGATATTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTTCAATGGATGATGTTAGTATTTTTTAAGAGATCCTCAAGGAACACAGTCAGAGAG
ATTTCATGGGTGCATTCTCTGCTCGTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCTGCC
ACACGGCAGACCTTCTCACCTCATCAGTATGATTCACTGGACTCTCCAGGGTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCTATTTAACCTGGTAAAGGCAGGGCTGG
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTAAATGGTCT
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAATTAAATTGTTCTGGTAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAAATGTTT
CTAAATAAAAATGTTAGTGGTTCCAATGGCTAATAAAAACAATTATTGTAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICGPNKCKCHPGYAGKTCNQDLNECGLKPRPC KHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGVVKQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHPKGNGTILKGDGTGNNNWPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIREKDNDLHWEPIRDPA GGQYLTVSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGLQVFVRKHGAALWGRNGGHGWRQTQI
TLRGADIKSEQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACCTTCCTTGCAACAGGTGCTGCTCGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATGGCTATTGAGAGACCCCA
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGGAAATACC
AACACAAGTTCACCATGATGCCACCCAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTCA
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGAGATTCATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCCCTGACATGCCATGTGGAAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTCAGTGAATTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTCGCTAGAAGTT
GCATCTGAGAAAGTAGGCCAGAACAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTACAGTTATCATCACTCCGTAGGACTGGAGAACGCTG
CACAGAAAAGGAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTGGATT
ATATCCATGTGTTCTTCTTCTATGGAAAAAAATATCAACCTACAAAGTTATAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGATCGGGCAAGATTGCACAGTACAGT
GTATGAAGTTATTGACGACATCCCTGCCAGCAGCAAGACCATCCAGAGT**TGA**ACTTCTG
GCTAACAGTACATTGAGTGAAATTCTGAAGAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAAGAACAGGACCAACACCTTACTCATTATTCCCTTACA
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAAGGTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCTCATAAGTTGTATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTGTGTTATTAAATTGTTATTAGTG
TTAAGAATGCTAAATTGTTCAATTGTTCAAATTCTATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAACATGCCTCTCTTTCAATCACC
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTGCTTTAAAAAAAAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDPPVTKPVVQIHP PSGAVEYVGNTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAA[ATGGCGCCCTCCGGAGTCTTGCAGTTCCCCTGGCAGTCCTGGTGCTGTT](#)
GCTTTGGGGTGT[CCCTGGACGCACGGGCGCGAGCAACGTTCGCGTCATCACGGACGAGA](#)
ACTGGAGAGAAC[TGCTGGAAGGAGACTGGATGATAGAATT](#)TTATGCCCGTGGTGCCTGCT
TGTCAA[AAATCTCAACCGAATGGAAAG](#)TTGCTGAATGGGAGAAGATCTGAGGTTAA
TATTGCGAA[AGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACG](#)TTATCATAACTGCTC
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAA[ACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAG](#)CCCCTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGG
TCAGGACGTGCCATAACTACTTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCTTGTCTTCAAAA[AGCGCAGACCACAGCCATACCCATACCC](#)CTTCAAAAAAAT
TATTATCAGAAC[CTGCACAAC](#)CTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTCA[GAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC](#)
CATAA[GACAACGCTCTGGGTCCATCATTGCCACAGATAAA](#)ACT[TAGTAA](#)ATTATAG
TTATCTTAATATTATGATTGATAAA[ACAGAACGATTGATCATTTGTTGTTGAAGTGA](#)
AACTGTGACTTTTGAA[ATTGCA](#)GGGTTCA[GTCAGTCTAGATTGT](#)CATTAAATTGAAGAGTCTA
CATTCA[GAAACATAAAAGCACTAGGT](#)TACAA[GTTGAA](#)ATTGATTAA[AGCACAGTATGATG](#)
GTTTAA[TAGTCTCTAATT](#)TTGAAAA[ACGTGCCAAGCAATAAGATT](#)TATGTTATTTGT
TTAATA[ATAACCTATTCAAGTCTGAG](#)TTGAAA[ATTACATT](#)CCCA[AGTATTG](#)CATTAT
TGAGGTATT[TAAGAAGATTATT](#)TAGAGAAA[ATTCTCATTG](#)ATATAATTCTCTG
TTCACTGTG[AAAAAAAGAAGATATT](#)CCCATAAA[ATTGGAGTTG](#)CCATTGTCTCAAG
AAATGTGATT[TCAGTGACAATT](#)CGTGGCTTTAGAGGTATATTCAA[AAATTCCCTGT](#)
ATT[TTTAGGTTATGCAACTAAT](#)AAA[ACTACCTTACATTAA](#)TTAATTACAGT[TTCTCACACA](#)
TGGTA[ATACAGGATATGCTACTGATTTAGGAAG](#)TTTAAGTT[CATGGTATTCTCTTGATTC](#)
CAACAA[AGTTGATTTCTCTGT](#)ATT[TTTCTTACTTACTATGGGT](#)TACATT[TTTATTTT](#)
CAAATTGGATGATAATT[CTTGGAAAC](#)ATT[TTTTATGTTAGTAAACAGT](#)ATT[TTTTGTT](#)
GTTTCAA[ACTGAAGTTACTGAGAGATCCAT](#)AA[ATTGAACAACTGTTG](#)TAATTAA[AAATT](#)
TTGCCACTTT[TCAGATTACATCATTCTGCTGAACTTCAACTTGAA](#)ATTGTTTT
TTCTTTGGATGT[GAAGGTGAA](#)ACATT[CCTGATT](#)TTGCTGATGT[GAAAAGCCTGGTA](#)
TTTACATT[TTGAA](#)ATT[CTCAAAGAAGCTTA](#)ATATAAA[AGTTGCATTCTACTCAGG](#)AAAAG
CATCTTCTTGTATATGCTTA[AAATGTATT](#)TTGCTCCTCATATACAGAA[AGTTCTTAATTGAT](#)
TTTACAGTCTGTA[ATGCTGATGTT](#)AAA[ATAACATT](#)TTTATATT[TTTAAAGACAA](#)
ACTTCATATT[ATTCCTGTTCTCCTGACTGGTA](#)ATATTG[GTGTTGGGATTTCACAGG](#)AAAA
GTCAGTAGGAT[GGAAC](#)ATT[TTTAGTGTATT](#)TTACTCCTTAA[AGAGCTAGA](#)ATACATAGTTT
CACCTTAA[AGAAGGGG](#)AAA[ATCATAAA](#)ATACAA[ATGAATCAACTGACC](#)ATTACGTA[GAGAC](#)
AATTCTGTA[ATGTCCCCT](#)TTCTAGGCTCTGTTGCTGTA[ATGTA](#)ATCCATTAGATTACAG
TATCGTA[ATATACAAGT](#)TTCTTAA[AGCCCTCTCCTT](#)AGAATTAA[AATTTGTA](#)CCATT
AAAGAGTTGGATGTGTA[ACTTGTGATGCCT](#)AGAAAA[ATATCCTAAGCACAA](#)AA[AAACT](#)
TTCTAAC[CACTTCATTAAAGCTG](#)AAAA[AAAAAAAAAAAAAA](#)

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGGGAGACCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTGTGCTAACCCAGTGGGACAGGGGGATTGGAAGAGCGGG
AAGTCCTGGCCCAGAGCAGTGTGACACTTCCCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGCCCTGGTTGGTGTCTGAGCTGTGCGAGGCCAAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTGTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAAGAGCTGGGCCAACAAAATGGAAGCCTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAACACAGACTGGCCTGCGCTGGAGGACCTGTGCTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGCGAGCGCAGTCTTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAACGCCGTATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GCCGCTGCCCTACAATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCCGCCCTGCTC
TCCCTGACCAAGCCACGAACGAGCTGGAGGAATCTCGGTA
CTTGAGGAGCTTAA
CTGAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAAAGGCA
TCTATGAGAGGCCTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGG
GAGGGTGTCAA
ACTGACACCCCGTAGACAGAAGAGGCTTTCTGTAGGTACACCATTGGCAA
CAGGGCCCCACAGCTGCTCATTGCCCTTCAAAGAGGAGGACGAGTGGACAGCCGCACA
TCGTCAGGTACTACGATGTCATGTGATGAGGAAATCGAGAGGATCAAGGAGATCGAAAAA
CCTAAACTTGACGAGCCACCCTGTGATCCCAAGACAGGAGTCCTCACTGTCGCCAGCTA
CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGGACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTA
ACTACATGAGTGTAGTGAAGCTG
GTGGTGCACCGTCTCCGTGATCTGGGCTGCAATTG
GGCTAAGAAGGGTACAGCTGTG
TTCTGGTACA
ACCTCTGCGGAGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCC
TGTGCTGTGGCTGCAAGTGGCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTGTGGATCAACAGAAGTTGACTTGACCATCCTTCTGTCCTCCCTTCTGGTC
CTTCAGCCCAGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCTGT
GTGACTGAAGTCCCAGCCCTCATTCA
GCCTGTGCCATCCCTGGCCCAAGGCTAGGATCA
AAAGTGGCTGCAGCAGAGTTAGCTGTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCA
GTGAACCAAAGTTCTGATACCTTGT
TACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACAAAAAATAAAATG
CCCTACCAAGAAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIWSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGEPLGTYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEATTTKSQVLDYLSYAVFQLGDLHRALELTRLLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDPYLPERDVYESLCRGEGVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMDSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCCTTTAGTGAAGACAGACCATAATCCAGTGTGAGTGAATTGATTGT
TTCATTATTACCGTTGGCTGGGGTAGTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTTGGGGATGCTGGTCTGGAGGCCAGCAGCGGGCCTTGCTCTGTCTTGCTCATGACCC
CAGGTTCTCTGGTTAAACTGAAAGCTACTACTGGCTGGGCCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTCGAGGCTGTAGGGAGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCGGATTGTCCCCACTACAGGGACCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCCGTGAGCGTTGCTGGCTGACCTCCCGAGCTACACTGTCCA
CTTGCCGTTGGCTGTGAACCGTACGGTGGCCATCACCTCCCTCGGTACTCTACTGGCAGGGGG
CCCAGGCTCCAGCAGGGATGAGGGCTCATGGGGATGAGCGGCCCTGGCTATGTCAGAGACCCCTGC
GCCACCTTACACACACTTGGGCCACTACGACTGGTTCTCATCATGCGAGATGACACATATGTGAGGCC
CCCCTGGCAGGCCCTGGCTGGCCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTCATTG
GGCAGGGCAGCAGGCCGTACTGTACGGGCTTGCTACCTGTTGTCACGGAGTCTCTGCTGCTCGTGC
GGCCACATCTGGATGGCTGGCAGGAGACATTCTCAGTGCCGTCCTGACGAGTGCTGGACGCTGCCATTG
ACTCTCTGGCGTGGCTGTCTCACAGCACCAGGGCAGCAGTATCGCTCATTTGAACACTGCCAAAATAGGG
ACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCCTCGCCGTGACCCCTGCTCCGAAGGTACCCATGT
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAGGGGAGGCCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACCAACTCTGGCTTGAGGTGCTGGGACTACTTCACAGAGCAGCACACCTCTCCGTGAGATGGGG
CTCCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGTGGGTATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCCTATCAGCCCGCTGCGCTTCCAGAACGAGCAGCGACTGCTCAACGGCTATCGCGCTTGACCCAGCAC
GGGGCATGGAGTACACCCCTGGACCTGCTGGAAATGTGTGACACAGCGTGGCACCGGCGGGCCCTGGCTCGA
GGTCAGCCTGCTGCGGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCAGTGAGGCCACCCGAGTGC
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGAGCCCGGCTTCCCTGAGGGCTTGCAGCCAATGTCC
TGGAGCCACGAGAACATGCAATTGCTACCCCTGTTGCTGGCTACGGGCACGAGAACGGTGGCGTGGAGCTCCAG
ACCCATTCTGGGGTAGAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCCTGGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGGGCCCTCCAGGTGCGACTCATGGACGTGGCTCGAAGAACCCCTGTGGACACTCTCT
TCTCCTTACCCCGTGTGACAAGGCTGGGCCAGTCTCAACCGCTGTGCGATGAATGCCATCTGGCT
GGCAGGCCCTTCCAGTCATTCCAGGAGTTCAATCCTGCCCTGTCAACACAGAGATACCCCCAGGGCCCC
CGGGGCTGGCCCTGACCCCCCTCCCTGGCTGACCCCTCCGGGGGCTCTATAGGGGGAGATTG
ACCGGCAGGCTCTGGGAGGGCTGCTTCTACACGCTGACTACCTGGCCGGCAGCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTTCTCCGGTTCTCAGGGCTCC
ACCTCTTCGGGCCGTAGAGCCAGGGCTGGTGCAGAACAGTTCTCCCTGCGAGACTGCAAGCCACGGCTCAGTGAAG
AACTTACCAACCGCTGCCGCTCAGCAACCTGGAGGGCTAGGGGGCGCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCGCTGGGGCCCTAACCTATTACCTTCTGTCTGCCAGCC
CCAGGAAGGGCAAGGAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRPHLDGCRG
DILSARPDEWLGRCLIDS LGVGCVSQHQQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGAEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTL DLLECVTQRGHRRALARRVSLRPLSRVEILPMPYVTEATRVQLVLPPLL
VAEAAAAPAFLEAFAAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTWTRPGPEVLRCRMNAISGWQAFFP
VHFQEFPALSPQRSPGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEALEGLEVMDVFLRFSGHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGC~~G~~CCAACGTGAGAGGAACCGTGC~~G~~GGCTGC~~G~~CTTCCTGTCCCCAAGCC
GTTCTAGAC~~G~~GGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG
AAGCATTTC~~T~~GTGCTTGATCACTATGCTAGGACACATTAGGATTGGTATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTACTGTATTATC~~T~~GTAAAACC
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACCAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACAACTG
GTTCTCCTTGCACGCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTAACAGCCTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTAGATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACGCCCTAGGGCATTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGTAATG
TGTTGGAAAGAAGTGTAAAGAATAATAATTGCAAATAACTATTAAATAATATTATAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAAATGTACAACAGCAACTAAAGAAA
ATTAAAGTGAAGTGA~~AA~~AT

FIGURE 120

MLSSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLLKKDPSPQFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGTCGATCTTACCAACAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTCCC~~AA~~ATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTCTCAGTGCCTGTTCATCACAGATGTGTTGACATTCGCAT
CTTCAAAACCTGTGATGAGAAAAGTTCAGCTACCTGAGAATTCACAGAGCTCCTGCT
ACAATTATGGATCAGGTTCAAGAATTGTTGCCATTGA~~ACT~~GGGAATATTTCAATCC
AGCTGCTACTTCTTTCTACTGACACCATTCC~~T~~GGCGTTAAGTTAAAGAACTGCTCAGC
CATGGGGCTCAC~~T~~GGTGGTTATCAACTCACAGGAGGAGCAGGAATTCC~~T~~ACAAGA
AACCTAAAATGAGAGAGTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGCCAAACAA
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAAACCCAAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTCGGATTGTGAAATGGTAGGAATAATCCTTG
AACAAAGGAAAATCTCTTAAGAACAGAAGGCACA~~ACT~~CAAATGTGAAAGAAGGAAGAGCA
AGAACATGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAAC~~T~~CAAAGGACTTC
ATAAGTATTGTTACTCTGATA~~CAA~~ATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAA
AA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTCGCCTCGGCTGACTTCTTCCTGCTGCTGCTTTCAGGGGCTGCGCTGATAAGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGCTTGACATCATTACGGATTCGC
AGACAAGTACCCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCTGTCAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTCAGTGAAGCCAGTGCACCCCTGTCTGTAGAGTGCAGGCTTACAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGACTGAGGAGCTGGGGCCACCCCCGGCTCACTACAGCTGATCGCAATGATGTACCTACTGCCACGGATT
CCAGGCCAATCCCAGATTCTGCAATTCTTCACTTAACACTCTGAAACAGGCACITGGTGTACTGCTG
TTCAAGGAGCAGACTGGCAGTACTACTGCATTGCTTCAATGACCGAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGAAATTATTGGGGGGTCTGGTGTCTGCTGTACTGCCCTGA
TCACGTTGGCATCTGCTGTGCATACAGACGTGGTACTTCATCAACAAACAGGATGGAGAAAGTACAAGA
ACCCAGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCAGTCAGACACAAGTCATGTTG
TGATCTGAGACCCGCGGTGGGCTGAGAGCGCACAGAGCAGTCAGACTCATTCAAGAGCTTTGCTTGGCCAAAGTTGACCA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAAGAGCTTTGCTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCAGAAACTGGGTGCGTTCACTGAGTTGGGTTCTAACTGTTCTGGCTGATTCCCGATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACGCCGTGCTGGCCCTGTGAAGGCCAGCATGTTACCAACTGGTCGT
CAGCAGCCACGACAGCACCATGTGAGATGGCAGGGTGGCTGGACAGCACAGCAGCGCATCCGGCGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATGGCCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC
TGATCGGTGTTGCACTGTTGAGCTTGGAGAAGCTTTGGATCAGCATTGTAACAAACAAAATCAGGAAG
GTAAATTGGGTGCTGGAAGAGGGATCTGCTGAGGAACCTGCTTGTCCAACAGGGTGTCAAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTATTATAAAATT
TACATCTAAATTGGTCAAGGATGTTGGATTATTGAAAAGAAAATTCTATTAAACTGTAACATATTGT
CATACAATGTTAAATAACCTATTGGTAAAGGAACTTCAACTTAAGGTTAGAAGTCTCAAGCTACTAGTGTAAAT
TGGAAAATATCAAATAATTAGAGTATTGGTACCCAGGAATCTCTCATGGAAAGTTACTGTGATGTTCTTCT
CACACAAGTTAGCCTTTCAACAGGAACCTCATCTGCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCCAGTTAACGCAATGTTGAAATCAGTTGCTCATCTCTCAAAAGAACCTCTCAGGTTAGCTTGAAC
GCCTTCTCTGAGATGACTAGGACAGTCTGTACCCAGAGGGCCACCCAGAAGGCCCTCAGATGTACATACAGATG
CCAGTCAGCTCTGGGGTGTGCCAGGCGCCCCGCTCTAGCTACTGTTGCTCGCTGTGCCAGGAGGCCCT
GCCATCCTGGCCCTGGCAGTGGCTGTGCTCCAGTGTAGCGTCCAGCTTGGGCTCTGTAACAGACCTCT
TCTCAGGTGGGACTGCAGGGACACTGGGTCTCCATGTAGCGTCCAGCTTGGGCTCTGTAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTGTTAAGTTGTTAATTATTGTT
AAGATTGCTAAGGCAAAGCAATTGCAAGTCTGCAAGTACAATAACATTAAAAGAAAATGGAT
CCCACGTCCCTTGCACAGAGAAAGCACCCAGCAGCCACAGGCTCTGTCGATTTCAAAACAAACATGAT
GGAGTGGCGGCCAGTCCAGCCTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGGGAGGAAAG
TGAAACGCCTGAATCAAAGCAGTTCTAATTGACTTAAATTCTATGCCCGGAGACACTGCTCCATT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTCAAGAGCAGGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTCTGTAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGCTGG
GAATGGCTCTCAACTCACCTTGTCTTCAGCTTCCAGTGTCTTGGTTTTATACTTTGACAGCTTTTT
AATTGCAATACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCCTGAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCCTCCCTGGTGTCTGCTGCATGGCATTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTCAAGCTCCAGCCTCCT
TCTTGGTTGTCAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTACACCTAAACCTTCTACACTAGTGC
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGACTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGGCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTGGCATTTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA